

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 ; Search time 3342.03 Seconds

(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-5

Perfect score: 651
Sequence: 1 atgaacggagcaataatag.....acaaaggaggaattcaatga 651

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_hgt: +
3: gb_in: +
4: gb_em: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_br: +
10: gb_ro: +
11: gb_ete: +
12: gb_ey: +
13: gb_un: +
14: gb_vl: +
15: em_ba: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_on: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_ete: +

28: em_un: +
29: em_vl: +
30: em_hgt_hum: +
31: em_hgt_inv: +
32: em_hgt_other: +
33: em_hgt_mus: +
34: em_hgt_pln: +
35: em_hgt_rtd: +
36: em_hgt_mam: +
37: em_hgt_vrt: +
38: em_ay: +
39: em_hgtg_hum: +
40: em_hgtg_mus: +
41: em_hgtg_other: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	651	6	BD245276
2	651	100.0	41401	7	AB009866
3	651	100.0	41708	6	BD245281
4	651	100.0	41708	6	AR368770
5	651	100.0	272850	1	AP004828
6	25	3.8	236256	2	AC130112
7	23	3.5	5169	3	AF298201
8	23	3.5	226995	2	BX372639
9	23	3.5	234851	5	BX005175
10	23	3.5	310003	1	AE014016
11	22	3.4	2473	8	SCYGR052W
12	22	3.4	4049	2	AC014940
13	22	3.4	4472	6	IND64927
14	22	3.4	6764	3	PPAPOLA
15	22	3.4	13449	6	AX346286
16	22	3.4	54812	8	YSCCHR1RAA
17	22	3.4	87841	8	AB005247
18	22	3.4	95906	9	AC008704
19	22	3.4	104685	9	AL589923
20	22	3.4	136240	3	AC117070
21	22	3.4	153550	2	BX001056
22	22	3.4	153550	2	AL354894
23	22	3.4	153607	2	AL355523
24	22	3.4	155321	2	AC116048
25	22	3.4	161517	9	AC009520
26	22	3.4	166113	2	AC016532
27	22	3.4	170136	9	AL356432
28	22	3.4	171653	9	AC080162
29	22	3.4	171670	2	AC110944
30	22	3.4	178357	2	AC018759
31	22	3.4	179722	2	AC131457
32	22	3.4	184359	10	AC121861
33	22	3.4	185269	2	AC073963

34	c	34	197611	9	AL390840	AL390840 Human DNA	91	21	3.2	178953	3	AC092400	AC092400 Drosophila
35	c	35	204056	9	AL160397	AL160397 Human DNA	92	21	3.2	182165	9	AC093429	AC093429 Homo sapi
36	c	36	210107	9	AL365214	AL365214 Human DNA	93	21	3.2	183866	2	BK855593	BK855593 Dario rer
37	c	37	217405	2	AC102588	AC102588 Mus muscu	94	21	3.2	183943	2	AC125506	AC125506 Papio anu
38	c	38	234081	3	PFMALP2	AL035475 Plasmodu	95	21	3.2	186308	9	AC026739	AC026739 Homo sapi
39	c	39	235497	2	AC094302	AC094302 Rattus no	96	21	3.2	186634	2	AC100722	AC100722 Mus muscu
40	c	40	241259	2	AC127409	AC127409 Rattus no	97	21	3.2	186717	9	CNS01DMR	AC100722 Mus muscu
41	c	41	248013	2	AC098092	AC098092 Rattus no	98	21	3.2	189505	9	AC092138	AC092138 Homo sapi
42	c	42	254398	2	AC137385	AC137385 Rattus no	99	21	3.2	192815	9	AC013444	AC013444 Homo sapi
43	c	43	302300	1	AP003186	AP003186 Clostridi	100	21	3.2	194832	2	AC025287	AC025287 Homo sapi
44	c	44	306037	1	AE014017	AE014017 Buchnera	101	21	3.2	197246	2	AC118774	AC118774 Homo sapi
45	c	45	325350	1	AP004823	AP004823 Staphyloc	102	21	3.2	197389	9	AL358791	AC118774 Homo sapi
46	c	46	438	6	BD269146	BD269146 Method fo	103	21	3.2	200364	10	AL844901	AL358791 Human DNA
47	c	47	530	11	GD0304	GD0304 S208PE427RE	104	21	3.2	207345	9	AC090962	AL844901 Mouse DNA
48	c	48	536	11	GD1464	GD1464 S208PE591RF	105	21	3.2	216161	9	AC024558	AC090962 Homo sapi
49	c	49	42430	3	AF003386	AF003386 Caenorhab	106	21	3.2	225956	2	BK842688	AC024558 Homo sapi
50	c	50	51590	2	AC145453	AC145453 Clcer art	107	21	3.2	231309	2	AC145303	BK842688 Dario rer
51	c	51	60232	1	AE001272	AE001272 Lactococc	108	21	3.2	237411	2	AC127402	AC145303 Mus muscu
52	c	52	63638	2	AC020175	AC020175 Drosophila	109	21	3.2	237983	2	AC138120	AC127402 Rattus no
53	c	53	75167	2	AC017342	AC017342 Drosophila	110	21	3.2	240144	3	AE003643	AC138120 Mus muscu
54	c	54	82854	10	AL626778	AL626778 Mouse DNA	111	21	3.2	249661	2	AC094299	AE003643 Drosophila
55	c	55	98492	8	AP006085	AP006085 Lotus cor	112	21	3.2	254946	2	AL844587	AC094299 Rattus no
56	c	56	104961	9	AC004075	AC004075 Homo sapi	113	21	3.2	257109	3	AC135577	AL844587 Dario rer
57	c	57	106277	9	AL359554	AL359554 Human DNA	114	21	3.2	267293	2	AC134614	AC135577 Dictyoste
58	c	58	112695	8	AC119418	AC119418 Medicago	115	21	3.2	275699	3	AE003649	AC134614 Mus muscu
59	c	59	116491	9	AC105942	AC105942 Homo sapi	116	21	3.2	295935	3	DR05ADH09	AE003649 Drosophila
60	c	60	121623	9	AC002412	AC002412 Homo sapi	117	21	3.2	305502	3	DR05ADH03	AE003409 Drosophila
61	c	61	126255	3	AY319931	AY319931 P. tritellonic	118	21	3.2	340552	3	PF929334	AL929335 Plasmodu
62	c	62	126781	2	AC016375	AC016375 Homo sapi	119	20	3.1	291	11	AU049248	AU049248 Rattus no
63	c	63	130043	8	AC126019	AC126019 Medicago	120	20	3.1	454	6	AX336874	AX336874 Sequence
64	c	64	135837	8	AC098693	AC098693 Oryza sat	121	20	3.1	492	6	BD244098	BD244098 Determina
65	c	65	135837	2	AC004837	AC004837 Homo sapi	122	20	3.1	696	8	AX121662	AX121662 Oryza sat
66	c	66	135873	2	AC012847	AC012847 Homo sapi	123	20	3.1	834	9	BC063494	BC063494 Homo sapi
67	c	67	138831	8	AC140005	AC140005 Oryza sat	124	20	3.1	1388	9	DB4107	DB4107 Homo sapien
68	c	68	142003	2	BX897661	BX897661 Dario rer	125	20	3.1	1474	9	DB4108	DB4107 Homo sapien
69	c	69	149273	10	AL928732	AL928732 Mouse DNA	126	20	3.1	1577	3	AX115445	AX115445 Sequence
70	c	70	153784	2	BX32589	BX32589 Dario rer	127	20	3.1	1594	9	DB4110	DB4110 Homo sapien
71	c	71	154259	9	AC013284	AC013284 Homo sapi	128	20	3.1	2126	8	MTL82	MTL82 Homo sapien
72	c	72	155353	2	BX323021	BX323021 Homo sapi	129	20	3.1	2668	6	AX835291	AX835291 Sequence
73	c	73	156100	2	AC011934	AC011934 Homo sapi	130	20	3.1	2668	6	AX098281	AX098281 Homo sapi
74	c	74	157482	3	AC092227	AC092227 Drosophila	131	20	3.1	2826	8	HNNHAG3D15	HNNHAG3D15 Sequence
75	c	75	157722	3	AC092248	AC092248 Drosophila	132	20	3.1	3965	9	AX124859	AX124859 Sunflower
76	c	76	158315	9	AL160267	AL160267 Human DNA	133	20	3.1	6137	2	AC147333	AC147333 Homo sapi
77	c	77	158630	2	AC124225	AC124225 Mus muscu	134	20	3.1	6196	8	CTR286093	CTR286093 Homo sapi
78	c	78	159369	2	AC119839	AC119839 Mus muscu	135	20	3.1	6775	6	AX458643	AX458643 Sequence
79	c	79	160302	2	AC068818	AC068818 Homo sapi	136	20	3.1	7689	3	DMT1MEL1	DMT1MEL1 Candida t
80	c	80	161304	2	AC061674	AC061674 Homo sapi	137	20	3.1	10176	3	AE001370	AE001370 Plasmodu
81	c	81	161341	2	AL929055	AL929055 Mus muscu	138	20	3.1	10575	2	AC017467	AC017467 Drosophila
82	c	82	162797	2	AC112974	AC112974 Mus muscu	139	20	3.1	10855	6	AX346391	AX346391 Sequence
83	c	83	164396	9	AC108034	AC108034 Homo sapi	140	20	3.1	11014	1	AE010501	AE010501 Fusedacte
84	c	84	164764	2	AC129624	AC129624 Homo sapi	141	20	3.1	11180	1	AF329100	AF329100 Bacteroid
85	c	85	167389	2	AC115926	AC115926 Mus muscu	142	20	3.1	11684	3	AE001403	AE001403 Plasmodu
86	c	86	168273	2	AC010812	AC010812 Homo sapi	143	20	3.1	13818	2	AC108445	AC108445 Homo sapi
87	c	87	171930	9	AL450334	AL450334 Human DNA	144	20	3.1	14335	6	AR408732	AR408732 Sequence
88	c	88	177130	2	AC019551	AC019551 Homo sapi	145	20	3.1	14335	6	AX067436	AX067436 Sequence
89	c	89	177293	2	AC146401	AC146401 Pan trogl	146	20	3.1	17691	3	CEP57A10	CEP57A10 Caenorhabdi
90	c	90	177865	9	AC098483	AC098483 Homo sapi	147	20	3.1	18005	8	LES312093	LES312093 Lycopersi

148	20	3.1	18585	6	AX281497	205	20	3.1	141529	2	AC108979	AC108979 Rattus no
149	20	3.1	21206	1	AE002104	206	20	3.1	142080	9	AC079748	AC079748 Homo sapi
150	20	3.1	28000	3	CEC15H7	207	20	3.1	142557	9	AL356499	AL356499 Human DNA
151	20	3.1	30225	3	CEP29C12	208	20	3.1	146286	9	AC027141	AC027141 Homo sapi
152	20	3.1	33650	3	CEK01A11	209	20	3.1	147098	9	AC008651	AC008651 Homo sapi
153	20	3.1	39897	2	AC020039	210	20	3.1	148109	8	AP003378	AP003378 Homo sapi
154	20	3.1	60923	2	AC091586	211	20	3.1	148978	2	AC134399	AC134399 Oryza sat
155	20	3.1	64263	9	AC132660	212	20	3.1	149169	5	AL840630	AL840630 Zebrafish
156	20	3.1	68719	2	AC106005	213	20	3.1	151162	2	AC025601	AC025601 Homo sapi
157	20	3.1	69674	9	AL136130	214	20	3.1	151843	2	AC009599	AC009599 Homo sapi
158	20	3.1	70392	2	AC079105	215	20	3.1	152595	2	AC140167	AC140167 Homo sapi
159	20	3.1	77273	8	AB022223	216	20	3.1	154199	2	BX321872	BX321872 Dantio rer
160	20	3.1	78167	2	AC023422	217	20	3.1	155047	2	AL390120	AL390120 Homo sapi
161	20	3.1	78341	8	F1003	218	20	3.1	155344	9	AC026407	AC026407 Homo sapi
162	20	3.1	79895	2	AC100317	219	20	3.1	155868	2	AC101929	AC101929 Mus muscu
163	20	3.1	80743	9	AL162402	220	20	3.1	155874	2	BX004782	BX004782 Homo sapi
164	20	3.1	81587	3	AF003135	221	20	3.1	156534	10	AC127552	AC127552 Mus muscu
165	20	3.1	84554	8	AC123571	222	20	3.1	157523	9	AC024106	AC024106 Homo sapi
166	20	3.1	84991	9	AC011424	223	20	3.1	158126	8	AP003245	AP003245 Oryza sat
167	20	3.1	86334	2	AC021610	224	20	3.1	158709	2	AC083827	AC083827 Homo sapi
168	20	3.1	88010	8	ATT14D3	225	20	3.1	159236	9	AC116158	AC116158 Homo sapi
169	20	3.1	96217	9	AL645729	226	20	3.1	159390	9	AC092823	AC092823 Homo sapi
170	20	3.1	97579	2	AC146722	227	20	3.1	159648	2	BX294128	BX294128 Dantio rer
171	20	3.1	99415	3	CEV54G11A	228	20	3.1	160925	8	AP004332	AP004332 Homo sapi
172	20	3.1	99859	2	AL159999	229	20	3.1	161474	2	AC144356	AC144356 Dantio rer
173	20	3.1	100288	2	AP001945	230	20	3.1	162436	2	AC083825	AC083825 Homo sapi
174	20	3.1	101047	9	AL365227	231	20	3.1	163179	9	AC022541	AC022541 Homo sapi
175	20	3.1	101466	9	AL450324	232	20	3.1	163576	10	AL807744	AL807744 Mouse DNA
176	20	3.1	102653	14	CYSOG	233	20	3.1	163970	3	AC010580	AC010580 Drosophila
177	20	3.1	110000	2	AL954766_2	234	20	3.1	164153	2	AC138835	AC138835 Homo sapi
178	20	3.1	110000	2	BX004762_0	235	20	3.1	164809	9	AC128690	AC128690 Homo sapi
179	20	3.1	110000	2	BX004762_3	236	20	3.1	165043	2	AC021432	AC021432 Homo sapi
180	20	3.1	110000	2	BX346444_00	237	20	3.1	165067	9	AL138927	AL138927 Human DNA
181	20	3.1	110000	2	PFYAL1.3_25	238	20	3.1	165330	10	AC087223	AC087223 Mus muscu
182	20	3.1	110000	10	AE014175_1	239	20	3.1	165392	2	AC011670	AC011670 Homo sapi
183	20	3.1	110261	9	AL807401	240	20	3.1	165693	9	AC087879	AC087879 Homo sapi
184	20	3.1	111182	9	AL359771	241	20	3.1	165870	9	AC025089	AC025089 Homo sapi
185	20	3.1	111767	8	F21E10	242	20	3.1	166462	2	AC138785	AC138785 Sus scrofa
186	20	3.1	111779	9	AL159988	243	20	3.1	166839	3	AL135931	AL135931 Homo sapi
187	20	3.1	112025	5	AL591418	244	20	3.1	167396	3	AC010579	AC010579 Drosophila
188	20	3.1	112424	9	HS1013A10	245	20	3.1	168066	2	AC026902	AC026902 Homo sapi
189	20	3.1	116521	9	HSJ65B22	246	20	3.1	168270	8	AC083943	AC083943 Homo sapi
190	20	3.1	120644	9	AC146041	247	20	3.1	169490	9	AC091910	AC091910 Homo sapi
191	20	3.1	121963	9	AL162397	248	20	3.1	169630	2	AC139788	AC139788 Homo sapi
192	20	3.1	122052	8	AC079633	249	20	3.1	170064	3	AC008323	AC008323 Drosophila
193	20	3.1	122889	9	HS0A204F4	250	20	3.1	171274	2	AC140166	AC140166 Homo sapi
194	20	3.1	123336	9	AC003075	251	20	3.1	171410	2	AC107689	AC107689 Mus muscu
195	20	3.1	123661	9	AC096661	252	20	3.1	171562	9	AC107027	AC107027 Homo sapi
196	20	3.1	125623	3	AC115599	253	20	3.1	172289	9	AC126767	AC126767 Homo sapi
197	20	3.1	125782	9	AC090365	254	20	3.1	172321	9	AC109631	AC109631 Homo sapi
198	20	3.1	126631	8	AP003379	255	20	3.1	172436	3	AC009751	AC009751 Drosophila
199	20	3.1	127039	2	AF252826	256	20	3.1	173288	2	BX640589	BX640589 Dantio rer
200	20	3.1	127039	2	AP001127	257	20	3.1	174143	5	AL929315	AL929315 Zebrafish
201	20	3.1	127677	9	AC102945	258	20	3.1	174189	2	AC145800	AC145800 Silurana
202	20	3.1	130583	2	AC007420	259	20	3.1	174701	2	AC007625	AC007625 Human DNA
203	20	3.1	130984	2	AC022766	260	20	3.1	175010	2	AC114587	AC114587 Mus muscu
204	20	3.1	132182	9	AC092916	261	20	3.1	176275	2	AC025551	AC025551 Homo sapi

c 262	20	3.1 177018	2	AC099716	Mus muscu	319	20	3.1 230827	2	AC130625	AC130625 Rattus no
c 263	20	3.1 178273	2	AC005308	Plasmodi	320	20	3.1 231647	2	AC114203	AC114203 Rattus no
c 264	20	3.1 178428	2	AL59185	Human DNA	321	20	3.1 231910	2	AC128365	AC128365 Rattus no
c 265	20	3.1 178761	2	AC132630	Rattus no	c 322	20	3.1 232323	2	AC127590	AC127590 Mus muscu
c 266	20	3.1 179173	10	AL669973	Mus DNA	323	20	3.1 233244	2	AC128266	AC128266 Rattus no
c 267	20	3.1 180225	9	AC104125	AC104125 Homo sapi	324	20	3.1 238560	2	AC114016	AC114016 Rattus no
c 268	20	3.1 180303	2	AC018969	AC018969 Homo sapi	c 325	20	3.1 240145	2	AC097778	AC097778 Rattus no
c 269	20	3.1 180461	1	AF250878	Salmonell	c 326	20	3.1 240288	2	BX37102	BX37102 Dantio rer
c 270	20	3.1 181166	9	AC087897	AC087897 Homo sapi	327	20	3.1 241570	2	AC125268	AC125268 Mus muscu
c 271	20	3.1 182020	9	AC113170	AC113170 Homo sapi	328	20	3.1 242416	2	AC133404	AC133404 Rattus no
c 272	20	3.1 183297	9	AC138804	BX511067 Dantio rer	329	20	3.1 244237	2	AC121060	AC121060 Rattus no
c 273	20	3.1 183410	2	BX511067	BX511067 Dantio rer	c 330	20	3.1 246199	2	AC119558	AC119558 Rattus no
c 274	20	3.1 184110	2	AC110532	AC110532 Mus muscu	331	20	3.1 246990	2	AC136583	AC136583 Rattus no
c 275	20	3.1 185967	2	AC113543	AC113543 Mus muscu	c 332	20	3.1 247151	2	AC098067	AC098067 Rattus no
c 276	20	3.1 186011	2	AC025826	AC025826 Homo sapi	c 333	20	3.1 247402	10	AC125187	AC125187 Rattus no
c 277	20	3.1 187516	2	AC138845	AC138845 Homo sapi	c 334	20	3.1 249943	3	AE014823	AE014823 Rattus no
c 278	20	3.1 189308	9	AC040896	AC040896 Homo sapi	c 335	20	3.1 250029	3	AE014816	AE014816 Rattus no
c 279	20	3.1 189709	9	AL160275	AL160275 Human DNA	336	20	3.1 250663	3	AE014826	AE014826 Rattus no
c 280	20	3.1 191108	9	AC140168	AC140168 Homo sapi	337	20	3.1 250906	2	AC123491	AC123491 Rattus no
c 281	20	3.1 191135	2	AC128919	AC128919 Rattus no	338	20	3.1 253120	2	AC097099	AC097099 Rattus no
c 282	20	3.1 191334	2	BX323462	BX323462 Dantio rer	339	20	3.1 253132	3	AE014846	AE014846 Rattus no
c 283	20	3.1 191775	2	AC074358	AC074358 Mus muscu	c 340	20	3.1 253772	2	AC109777	AC109777 Rattus no
c 284	20	3.1 192550	2	AC026103	AC026103 Homo sapi	c 341	20	3.1 253924	3	AE014822	AE014822 Rattus no
c 285	20	3.1 193029	2	AL355594	AL355594 Homo sapi	c 342	20	3.1 255434	2	AC130154	AC130154 Rattus no
c 286	20	3.1 193444	8	AF229199	AF229199 Oryza sat	c 343	20	3.1 257453	2	AC128972	AC128972 Rattus no
c 287	20	3.1 194149	9	AC100799	AC100799 Homo sapi	c 344	20	3.1 257727	2	AC138616	AC138616 Rattus no
c 288	20	3.1 194287	10	AL672015	AL672015 Mouse DNA	c 345	20	3.1 262050	1	AP000985	AP000985 Sulfolobu
c 289	20	3.1 195607	2	AC117567	AC117567 Mus muscu	c 346	20	3.1 264902	2	AC005158	AC005158 Homo sapi
c 290	20	3.1 195906	2	AC136746	AC136746 Mus muscu	c 347	20	3.1 266344	9	AC005158	AC005158 Rattus no
c 291	20	3.1 196243	2	AC127471	AC127471 Sus scrofa	c 348	20	3.1 267183	2	AC127079	AC127079 Rattus no
c 292	20	3.1 196315	2	AC118093	AC118093 Rattus no	349	20	3.1 268074	2	AC126999	AC126999 Rattus no
c 293	20	3.1 196640	2	AC026009	AC026009 Homo sapi	350	20	3.1 271932	2	AC097673	AC097673 Rattus no
c 294	20	3.1 197181	2	BX547937	BX547937 Dantio rer	351	20	3.1 274015	2	AC127795	AC127795 Rattus no
c 295	20	3.1 197206	2	AC023757	AC023757 Homo sapi	352	20	3.1 274855	2	BX511168	BX511168 Dantio rer
c 296	20	3.1 197295	9	AC073585	AC073585 Homo sapi	353	20	3.1 279110	1	RPX003	RPX003 Rattus no
c 297	20	3.1 197646	2	AC011041	AC011041 Homo sapi	c 354	20	3.1 281743	1	AC113873	AC113873 Rattus no
c 298	20	3.1 199294	10	AL589652	AL589652 Mouse DNA	c 355	20	3.1 290433	1	AE017034	AE017034 Rattus no
c 299	20	3.1 199510	2	AC103122	AC103122 Rattus no	356	20	3.1 294307	2	AC093974	AC093974 Rattus no
c 300	20	3.1 199724	10	AL808111	AL808111 Mouse DNA	c 357	20	3.1 296836	2	AC095624	AC095624 Rattus no
c 301	20	3.1 201437	2	AC015981	AC015981 Homo sapi	c 358	20	3.1 298836	2	AC095624	AC095624 Rattus no
c 302	20	3.1 203111	2	AP001647	AP001647 Homo sapi	359	20	3.1 300853	2	AC135145	AC135145 Rattus no
c 303	20	3.1 204652	2	PFMAL13P6	AL049183 Plasmodi	c 360	20	3.1 304674	3	AE003579	AE003579 Rattus no
c 304	20	3.1 205239	2	AC140177	AC140177 Homo sapi	361	20	3.1 308331	2	AC107110	AC107110 Rattus no
c 305	20	3.1 207303	2	AL645562	AL645562 Pan trogl	c 362	20	3.1 313096	2	AC131879	AC131879 Rattus no
c 306	20	3.1 211305	9	AC009975	AC009975 Homo sapi	363	20	3.1 324367	8	AE017091	AE017091 Rattus no
c 307	20	3.1 215896	2	AC046180	AC046180 Homo sapi	c 364	20	3.1 332760	2	AC147293	AC147293 Rattus no
c 308	20	3.1 216422	2	AC096528	AC096528 Rattus no	c 365	20	3.1 335799	2	BX005139	BX005139 Pan trogl
c 309	20	3.1 216972	9	AC067819	AC067819 Homo sapi	c 366	20	3.1 340801	2	AC006751	AC006751 Caenorhab
c 310	20	3.1 217332	2	BX572077	BX572077 Dantio rer	c 367	20	3.1 349980	6	AX344550	AX344550 Sequence
c 311	20	3.1 218160	1	STYPRKCH1	AL513383 Salmonell	c 368	19	2.9 390	6	YSKRELA	YSKRELA Candida alb
c 312	20	3.1 220665	2	AC123017	AC123017 Rattus no	369	19	2.9 393	3	AY297308	AY297308 Jolles sp
c 313	20	3.1 222002	2	AC130398	AC130398 Rattus no	c 370	19	2.9 414	3	AF328032	AF328032 Ruffles sp
c 314	20	3.1 223102	2	AC094457	AC094457 Rattus no	c 371	19	2.9 468	4	BTHAUC39	BTHAUC39 Sequence
c 315	20	3.1 223728	2	AC097906	AC097906 Rattus no	c 372	19	2.9 471	6	AX510116	AX510116 Sequence
c 316	20	3.1 224098	2	AC111386	AC111386 Rattus no	c 373	19	2.9 507	6	AR414869	AR414869 Sequence
c 317	20	3.1 226793	3	AE003753	AE003753 Drosophill	c 374	19	2.9 507	6	BD110422	BD110422 EST and e
c 318	20					c 375	19	2.9 530	11	G97907	G97907 S208P6003FC

376	19	2.9	622	12	AY199254	AY199254 Arabidops	c 433	19	2.9	19787	6	AX346353	AX346353 Sequence
377	19	2.9	629	5	AY206472	AY206472 Rana cete	434	19	2.9	24592	2	AC013944	AC013944 Drosophil
378	19	2.9	677	11	BV060604	BV060604 S212P6595	435	19	2.9	27223	3	AF068720	AF068720 Caenorhab
c 379	19	2.9	649	11	GS1055	GS1055 SHGC-79694	c 436	19	2.9	30804	9	AC134338	AC134338 Homo sapi
c 380	19	2.9	689	11	GS1339	GS1339 SHGC-85495	c 437	19	2.9	31883	3	U80455	U80455 Caenorhabd1
c 381	19	2.9	753	6	AX185792	AX185792 Sequence	c 438	19	2.9	32310	3	CER34D10	CER34D10
c 382	19	2.9	850	8	AJ590798	AJ590798 Arabidops	c 439	19	2.9	34335	9	AC112711	AC112711 Homo sapi
c 383	19	2.9	988	14	HBVPV2A	L59989 Rice hoja b	c 440	19	2.9	36729	2	AC014489	AC014489 Drosophil
c 384	19	2.9	1197	1	AF188102	AF188102 Lactococc	c 441	19	2.9	37034	2	AC066581	AC066581 Homo sapi
c 385	19	2.9	1295	5	AF176818	AF176818 Siliurana	c 442	19	2.9	37071	2	AC141537	AC141537 Rattus no
c 386	19	2.9	1416	3	AK115479	AK115479 Clona Int	c 443	19	2.9	37140	9	AY177663	AY177663 Homo sapi
c 387	19	2.9	1526	8	AY084425	AY084425 Arabidops	c 444	19	2.9	38482	3	U28736	U28736 Caenorhabd1
c 388	19	2.9	1530	8	AF324664	AF324664 Arabidops	c 445	19	2.9	38980	3	CER06C1	CER06C1
c 389	19	2.9	1550	8	AF327427	AF327427 Arabidops	c 446	19	2.9	39065	2	AC068331	AC068331 Homo sapi
c 390	19	2.9	1799	8	ATHG3P	L14749 Arabidops	c 447	19	2.9	39282	9	AC005596	AC005596 Homo sapi
c 391	19	2.9	1833	8	U43593	U43593 Arabidops	c 448	19	2.9	39491	10	AC004101	AC004101
c 392	19	2.9	2004	6	AX461330	AX461330 Sequence	c 449	19	2.9	40016	9	AC003038	AC003038 Homo sapi
c 393	19	2.9	2324	5	XELMRP1B	M34895 X. laevis ne	c 450	19	2.9	41830	10	AC005520	AC005520 Homo sapi
c 394	19	2.9	2677	8	AF383151	AF383151 Manihoc e	c 451	19	2.9	42613	3	AF106575	AF106575 Caenorhab
c 395	19	2.9	2807	3	AF313771	AF313771 Drosophil	c 452	19	2.9	44430	8	AC021046	AC021046 Arabidops
c 396	19	2.9	2877	3	SC2P52AA	M63342 S. pallida o	c 453	19	2.9	46422	8	OSJN00249	OSJN00249
c 397	19	2.9	2978	3	SC2P18AA	M63342 S. pallida o	c 454	19	2.9	49197	8	AP006349	AP006349 Lotus cor
c 398	19	2.9	3113	8	ATU43322	U43322 Arabidops	c 455	19	2.9	50440	2	AC140105	AC140105
c 399	19	2.9	3620	14	HBVPV2R	L54073 Rice hoja b	c 456	19	2.9	50879	8	OSJN00283	OSJN00283
c 400	19	2.9	4444	8	DCINUC1	X78423 D. carota (Q	c 457	19	2.9	51305	9	AL691465	AL691465 Homo sapi
c 401	19	2.9	4598	14	ACU04051	U04051 Autographa	c 458	19	2.9	52007	2	AC080151	AC080151
c 402	19	2.9	4962	8	AF180896	AF180896 Arabidops	c 459	19	2.9	52478	10	AL672172	AL672172 Homo sapi
c 403	19	2.9	5032	6	AX251778	AX251778 Sequence	c 460	19	2.9	58473	9	AL449103	AL449103 Homo sapi
c 404	19	2.9	5171	3	AF449198	AF449198 Plasmodiu	c 461	19	2.9	59865	2	AC133641	AC133641 Homo sapi
c 405	19	2.9	5219	4	BOVME5A	M95684 Bos taurus	c 462	19	2.9	59865	2	AC133641	AC133641 Homo sapi
c 406	19	2.9	6061	6	AX345043	AX345043 Sequence	c 463	19	2.9	59918	2	AC133641	AC133641 Homo sapi
c 407	19	2.9	6179	6	AX251097	AX251097 Sequence	c 464	19	2.9	60747	9	AL355487	AL355487 Homo sapi
c 408	19	2.9	6179	6	AX344246	AX344246 Sequence	c 465	19	2.9	61615	9	AC068779	AC068779 Homo sapi
c 409	19	2.9	6391	6	AX323524	AX323524 Sequence	c 466	19	2.9	64071	2	AC084122	AC084122 Homo sapi
c 410	19	2.9	6655	6	AX277840	AX277840 Sequence	c 467	19	2.9	65784	5	BX511238	BX511238 Zebrafish
c 411	19	2.9	6665	6	AX323515	AX323515 Sequence	c 468	19	2.9	67970	2	PFMA11P3	PFMA11P3
c 412	19	2.9	6665	6	AX344984	AX344984 Sequence	c 469	19	2.9	70562	2	AC120033	AC120033 Homo sapi
c 413	19	2.9	6802	6	AX346132	AX346132 Sequence	c 470	19	2.9	71571	10	BX530028	BX530028 Mouse DNA
c 414	19	2.9	8323	6	AX344961	AX344961 Sequence	c 471	19	2.9	72383	2	AC101173	AC101173 Mus muscu
c 415	19	2.9	8334	14	LMPDDR	L34213 Fish lympho	c 472	19	2.9	72902	8	ATAC015985	ATAC015985
c 416	19	2.9	8530	3	TET491316	AJ491316 Tetrahyme	c 473	19	2.9	73007	9	AL606809	AL606809 Zebrafish
c 417	19	2.9	8597	8	AF126285	AF126285 Pleurotus	c 474	19	2.9	73260	5	AL606809	AL606809 Zebrafish
c 418	19	2.9	9879	8	AF126285	AF126285 Pleurotus	c 475	19	2.9	73260	5	AL606809	AL606809 Zebrafish
c 419	19	2.9	10599	1	AE007589	AE007589 Clostridi	c 476	19	2.9	73491	9	AY246560	AY246560 Homo sapi
c 420	19	2.9	11046	1	U32764	U32764 Haemophilus	c 477	19	2.9	76396	2	AC012995	AC012995 Drosophil
c 421	19	2.9	11363	1	AF335469	AF335469 Escherich	c 478	19	2.9	76763	9	AL157705	AL157705 Homo sapi
c 422	19	2.9	11496	1	AE006137	AE006137 Pasteurel	c 479	19	2.9	80601	9	AL1591472	AL1591472 Homo sapi
c 423	19	2.9	12132	1	AE000595	AE000595 Helicobac	c 480	19	2.9	80666	2	AC139531	AC139531 Homo sapi
c 424	19	2.9	12426	6	AX251236	AX251236 Sequence	c 481	19	2.9	81057	9	AC080125	AC080125 Homo sapi
c 425	19	2.9	13376	6	AX345485	AX345485 Sequence	c 482	19	2.9	82952	9	AC080125	AC080125 Homo sapi
c 426	19	2.9	14887	6	AX345533	AX345533 Sequence	c 483	19	2.9	86523	3	AC084196	AC084196 Caenorhab
c 427	19	2.9	15267	3	AY191994	AY191994 Fugu rubr	c 484	19	2.9	86997	2	AC108364	AC108364 Pan trogl
c 428	19	2.9	15511	5	FRU131394	AJ131394 Sequence	c 485	19	2.9	87538	9	AL158200	AL158200 Homo sapi
c 429	19	2.9	17294	6	AX345888	AX345888 Sequence	c 486	19	2.9	89261	9	AC098863	AC098863 Homo sapi
c 430	19	2.9	17934	6	AX346621	AX346621 Sequence	c 487	19	2.9	89479	8	AC006932	AC006932 Genomic s
c 431	19	2.9	18817	6	AX281383	AX281383 Sequence	c 488	19	2.9	91203	9	AC096731	AC096731 Homo sapi
c 432	19	2.9	18817	6	AX346593	AX346593 Sequence	c 489	19	2.9	94399	8	AC111015	AC111015 Oryza sat

C 490	19	2.9	95173	8	AC068324	AC068324 Arabidops	547	19	2.9	120952	9	AC005053	AC005053 Homo sapi
491	19	2.9	96180	9	AC005868	AC005868 Homo sapi	C 548	19	2.9	121068	9	AC015876	AC015876 Homo sapi
492	19	2.9	96618	9	HS34761	AL030570 Human DNA	C 549	19	2.9	121372	2	AC145851	AC145851 Dasyatis n
493	19	2.9	98210	2	AC102834	AC102834 Mus muscu	550	19	2.9	121763	2	AC147012	AC147012 Medicago
494	19	2.9	98917	2	AC116753	AC116753 Mus muscu	C 551	19	2.9	121766	2	AC016019	AC016019 Homo sapi
495	19	2.9	101500	9	AL365505	AL365505 Human DNA	C 552	19	2.9	121959	9	AF536523	AF536523 Drosophila
496	19	2.9	102488	9	AP005231	AP005231 Homo sapi	C 553	19	2.9	124359	9	AL157936	AL157936 Homo sapi
497	19	2.9	103041	9	AC093384	AC093384 Homo sapi	C 554	19	2.9	125047	2	AC146988	AC146988 Homo sapi
498	19	2.9	103563	9	AC006979	AC006979 Homo sapi	C 555	19	2.9	125419	9	HS1658114	HS1658114 Arabidops
499	19	2.9	103942	9	AC009449	AC009449 Homo sapi	556	19	2.9	125429	9	AC084291	AC084291 Homo sapi
500	19	2.9	103942	2	AC091859	AC091859 Homo sapi	C 557	19	2.9	125634	2	AC141713	AC141713 Homo sapi
501	19	2.9	103966	8	AC125473	AC125473 Medicago	558	19	2.9	125919	2	AC146630	AC146630 Homo sapi
C 502	19	2.9	105582	2	AC139065	AC139065 Homo sapi	C 559	19	2.9	126181	9	AC074131	AC074131 Homo sapi
C 503	19	2.9	106034	9	AC134028	AC134028 Homo sapi	C 560	19	2.9	126342	2	AC010224	AC010224 Homo sapi
C 504	19	2.9	106346	9	AC004045	AC004045 Homo sapi	C 561	19	2.9	126386	8	AC0005169	AC0005169 Homo sapi
C 505	19	2.9	107214	8	AC0043178	AC0043178 Arabidops	C 562	19	2.9	127718	9	BS000059	BS000059 Pen trogl
C 506	19	2.9	107977	2	AC136681	AC136681 Homo sapi	C 563	19	2.9	128465	2	AC138569	AC138569 Homo sapi
507	19	2.9	108916	9	AC010450	AC010450 Homo sapi	564	19	2.9	128710	9	HS111920	HS111920 Homo sapi
C 508	19	2.9	109359	9	AC004857	AC004857 Homo sapi	C 565	19	2.9	128907	9	AC105443	AC105443 Homo sapi
509	19	2.9	110000	2	AC107252_3	Continuation (4 of	566	19	2.9	129949	2	AC022940	AC022940 Homo sapi
510	19	2.9	110000	2	AC110642_2	Continuation (3 of	C 567	19	2.9	131005	5	AL929282	AL929282 Arabidops
511	19	2.9	110000	2	AC119727_2	Continuation (3 of	C 568	19	2.9	131250	8	AC128645	AC128645 Homo sapi
C 512	19	2.9	110000	2	AL137126_0	AL137126 Homo sapi	569	19	2.9	131274	9	AC069506	AC069506 Homo sapi
513	19	2.9	110000	2	AL672265_0	AL672265 Homo sapi	570	19	2.9	131278	2	AC108753	AC108753 Homo sapi
C 514	19	2.9	110000	2	BX323883_0	BX323883 Homo sapi	C 571	19	2.9	131526	14	AT145471	AT145471 Arabidops
C 515	19	2.9	110000	2	BK470178_0	BK470178 Danto rer	572	19	2.9	132010	2	AC024351	AC024351 Homo sapi
516	19	2.9	110000	2	PFMAL13_07	Continuation (8 of	573	19	2.9	132604	6	AA8542	AA8542 Sequence 1
517	19	2.9	110000	2	PFMAL13_07	Continuation (8 of	C 574	19	2.9	133894	6	AA8542	AA8542 Sequence 1
518	19	2.9	110000	2	PFMAL13_08	Continuation (8 of	C 575	19	2.9	133894	14	122858	122858 Arabidops
519	19	2.9	110000	3	PFMAL13_08	Continuation (8 of	C 576	19	2.9	134242	9	AL607128	AL607128 Homo sapi
C 520	19	2.9	110000	3	AC116505_0	AC116505 Dicyoste	C 577	19	2.9	135014	8	AP003222	AP003222 Homo sapi
C 521	19	2.9	110000	3	AC116557_1	Continuation (2 of	578	19	2.9	135146	2	AC087562	AC087562 Pen trogl
C 522	19	2.9	110000	3	AC116584_4	Continuation (5 of	C 579	19	2.9	135310	2	AC146087	AC146087 Homo sapi
523	19	2.9	110000	6	AR274513_08	Continuation (9 of	C 580	19	2.9	135585	8	AC118134	AC118134 Homo sapi
524	19	2.9	110000	6	AR409405_1	Continuation (2 of	C 581	19	2.9	135599	8	CPU30821	CPU30821 Homo sapi
525	19	2.9	110000	6	BD061520_1	Continuation (2 of	C 582	19	2.9	136175	8	AP004656	AP004656 Homo sapi
526	19	2.9	110000	10	AE008681_0	AE008681 Mus muscu	C 583	19	2.9	136729	10	AC136023	AC136023 Homo sapi
527	19	2.9	110000	10	AE008681_0	AE008681 Mus muscu	C 584	19	2.9	140244	2	AC119962	AC119962 Homo sapi
528	19	2.9	110074	2	AC147364	AC147364 Medicago	C 585	19	2.9	140801	10	AC124701	AC124701 Homo sapi
529	19	2.9	110352	8	AC006220	AC006220 Arabidops	C 586	19	2.9	141361	2	AC136524	AC136524 Homo sapi
C 530	19	2.9	111117	2	AL358932	AL358932 Homo sapi	587	19	2.9	141790	10	AL671759	AL671759 Homo sapi
531	19	2.9	111201	9	AC108217	AC108217 Homo sapi	C 588	19	2.9	142125	2	AC129835	AC129835 Homo sapi
C 532	19	2.9	111535	10	AL928867	AL928867 Homo sapi	C 589	19	2.9	143502	2	AC136225	AC136225 Homo sapi
533	19	2.9	111809	9	AC072041	AC072041 Homo sapi	C 590	19	2.9	143701	9	HS29C18	HS29C18 Homo sapi
534	19	2.9	112022	10	BK537149	BK537149 Homo sapi	C 591	19	2.9	143756	9	AC136365	AC136365 Homo sapi
C 535	19	2.9	112316	9	AC080079	AC080079 Homo sapi	592	19	2.9	143834	9	AC004960	AC004960 Homo sapi
C 536	19	2.9	112685	2	AC016592	AC016592 Homo sapi	C 593	19	2.9	144060	2	AC132074	AC132074 Homo sapi
C 537	19	2.9	113199	9	AC126014	AC126014 Medicago	594	19	2.9	144362	8	AP005112	AP005112 Homo sapi
538	19	2.9	113656	9	AC112253	AC112253 Homo sapi	595	19	2.9	144898	2	AC135189	AC135189 Homo sapi
539	19	2.9	113840	9	AC117421	AC117421 Homo sapi	596	19	2.9	145285	2	AC102291	AC102291 Homo sapi
540	19	2.9	113880	3	PFMAL1P4	AL008670 Plasmiditu	597	19	2.9	145309	2	AC073414	AC073414 Homo sapi
541	19	2.9	114626	4	AC138157	AC138157 Carollia	598	19	2.9	145424	9	AC010602	AC010602 Homo sapi
542	19	2.9	117289	2	AL512309	AL512309 Homo sapi	C 599	19	2.9	145614	2	AC006872	AC006872 Homo sapi
C 543	19	2.9	118591	2	AC020202	AC020202 Drosophila	C 600	19	2.9	145655	8	AP003546	AP003546 Homo sapi
C 544	19	2.9	119696	2	AP005563	AP005563 Oryza sat	C 601	19	2.9	146000	9	AP005433	AP005433 Homo sapi
C 545	19	2.9	119701	5	BX247898	BX247898 Zebrafish	602	19	2.9	146039	5	AL627132	AL627132 Zebrafish
546	19	2.9	120368	9	AF257498	AF257498 Homo sapi	603	19	2.9	146244	2	AP002083	AP002083 Homo sapi

604	19	2.9	146568	BK470073	Zebrafish	c	661	19	2.9	160432	5	AL929072	Zebrafish	AL929072	Zebrafish
c 605	19	2.9	146712	5	AL935136	AL935136	662	19	2.9	160580	5	AC116162	AC116162	Hom sapi	AC116162
c 606	19	2.9	146806	2	AC142093	Canis fam	663	19	2.9	160732	9	AC018647	AC018647	Hom sapi	AC018647
c 607	19	2.9	146945	9	AC009464	Hom sapi	664	19	2.9	160812	2	BK470210	BK470210	Danio rer	BK470210
c 608	19	2.9	147208	5	BK470202	Zebrafish	665	19	2.9	160872	2	AC026560	AC026560	Hom sapi	AC026560
c 609	19	2.9	147640	2	AP003542	AP003542	666	19	2.9	161250	8	AC079634	AC079634	Genomic S	AC079634
c 610	19	2.9	147686	10	AC124369	AC124369	667	19	2.9	161365	10	AC122505	AC122505	Mus muscu	AC122505
c 611	19	2.9	147920	2	BK649497	BK649497	668	19	2.9	161532	9	AC146202	AC146202	Pan trogl	AC146202
c 612	19	2.9	148022	2	AL137838	AL137838	669	19	2.9	161664	9	UB8296	UB8296	Hom sapien	UB8296
c 613	19	2.9	148263	9	AC091988	Hom sapi	670	19	2.9	161812	5	BK005045	BK005045	Zebrafish	BK005045
c 614	19	2.9	148804	2	AC138732	Pongo pyg	c 671	19	2.9	161946	9	AC094014	AC094014	Papio anu	AC094014
c 615	19	2.9	148820	2	AC128050	Rattus no	672	19	2.9	162513	10	AC132145	AC132145	Mus muscu	AC132145
c 616	19	2.9	148906	2	AP003629	AP003629	673	19	2.9	162753	2	AC144197	AC144197	Mus muscu	AC144197
c 617	19	2.9	149560	2	BK255929	BK255929	674	19	2.9	162859	2	AC021369	AC021369	Mus muscu	AC021369
c 618	19	2.9	150207	2	AL451067	AL451067	c 675	19	2.9	163246	2	AC120248	AC120248	Rattus no	AC120248
c 619	19	2.9	150879	2	AC134277	AC134277	c 676	19	2.9	163353	10	AL627076	AL627076	Mus muscu	AL627076
c 620	19	2.9	150922	8	AP004568	AP004568	c 677	19	2.9	163419	8	AP002908	AP002908	Human DNA	AP002908
c 621	19	2.9	151006	2	AC025893	AC025893	c 678	19	2.9	163459	9	AL139821	AL139821	Human DNA	AL139821
c 622	19	2.9	151106	2	BK465183	BK465183	c 679	19	2.9	163747	9	AC146255	AC146255	Pan trogl	AC146255
c 623	19	2.9	151248	2	BK511002	BK511002	c 680	19	2.9	163891	2	AC091264	AC091264	Hom sapi	AC091264
c 624	19	2.9	151253	5	BK649371	BK649371	c 681	19	2.9	164083	9	AC011034	AC011034	Hom sapi	AC011034
c 625	19	2.9	151778	9	AC021311	AC021311	c 682	19	2.9	164167	2	AC090104	AC090104	Hom sapi	AC090104
c 626	19	2.9	151966	9	AC009901	AC009901	c 683	19	2.9	164372	2	AL844602	AL844602	Mus muscu	AL844602
c 627	19	2.9	152196	2	BK548040	BK548040	c 684	19	2.9	164519	9	AC020630	AC020630	Hom sapi	AC020630
c 628	19	2.9	153338	2	AP005907	AP005907	c 685	19	2.9	164554	2	AC084811	AC084811	Hom sapi	AC084811
c 629	19	2.9	153829	2	AC141671	Ap1a mell	c 686	19	2.9	164739	2	BK682456	BK682456	Hom sapi	BK682456
c 630	19	2.9	153854	2	AC136202	Bos tauru	c 687	19	2.9	164830	4	AC144690	AC144690	Didelphis	AC144690
c															

c 718	19	2.9 171580	2	AC119887	AC119887 Mus muscu	c 775	19	2.9 180759	2	AC102274	AC102274 Mus muscu
c 719	19	2.9 171924	2	AC101861	AC101861 Mus muscu	c 776	19	2.9 180816	2	AC113230	AC113230 Sus scrofa
c 720	19	2.9 171969	2	BX255960	BX255960 Dantio rer	c 777	19	2.9 181085	2	AC114419	AC114419 Mus muscu
c 721	19	2.9 172003	8	AP002910	AP002910 Oryza sat	c 778	19	2.9 181250	2	BX571794	BX571794 Dantio rer
c 722	19	2.9 172043	9	AC026797	AC026797 Homo sapi	c 779	19	2.9 181308	9	AL153148	AL153148 Human DNA
c 723	19	2.9 172557	2	AC018944	AC018944 Homo sapi	c 780	19	2.9 181899	2	AC015904	AC015904 Homo sapi
c 724	19	2.9 172808	2	AC146379	AC146379 Pan trogl	c 781	19	2.9 181904	2	AC027623	AC027623 Homo sapi
c 725	19	2.9 172918	5	BX323457	BX323457 Zebrafish	c 782	19	2.9 181928	9	AC099674	AC099674 Homo sapi
c 726	19	2.9 173192	5	AL929030	AL929030 Zebrafish	c 783	19	2.9 181964	2	AC129023	AC129023 Mus muscu
c 727	19	2.9 173256	2	BX005207	BX005207 Dantio rer	c 784	19	2.9 182105	2	AC036149	AC036149 Homo sapi
c 728	19	2.9 173398	2	AC092972	AC092972 Homo sapi	c 785	19	2.9 182660	2	AC012415	AC012415 Homo sapi
c 729	19	2.9 173585	2	BX571679	BX571679 Dantio rer	c 786	19	2.9 182810	10	BX284626	BX284626 Homo sapi
c 730	19	2.9 173962	9	AF274856	AF274856 Homo sapi	c 787	19	2.9 183001	2	AC114227	AC114227 Rattus no
c 731	19	2.9 174074	2	BX842671	BX842671 Mus muscu	c 788	19	2.9 183066	9	AC021549	AC021549 Homo sapi
c 732	19	2.9 174383	9	AL929216	AL929216 Zebrafish	c 789	19	2.9 183093	9	AC138688	AC138688 Homo sapi
c 733	19	2.9 174399	9	AC104576	AC104576 Homo sapi	c 790	19	2.9 183105	3	AC104606	AC104606 Drosophila
c 734	19	2.9 174423	2	AC141189	AC141189 Rattus no	c 791	19	2.9 183168	9	AC092181	AC092181 Homo sapi
c 735	19	2.9 174632	2	BX897657	BX897657 Dantio rer	c 792	19	2.9 183196	2	AC083924	AC083924 Homo sapi
c 736	19	2.9 174654	9	AC073167	AC073167 Homo sapi	c 793	19	2.9 183508	2	AC131086	AC131086 Mus muscu
c 737	19	2.9 174725	5	AL954317	AL954317 Zebrafish	c 794	19	2.9 183544	10	AC102132	AC102132 Mus muscu
c 738	19	2.9 174893	3	AC104608	AC104608 Drosophila	c 795	19	2.9 183696	9	AC008172	AC008172 Homo sapi
c 739	19	2.9 175028	9	AC066692	AC066692 Homo sapi	c 796	19	2.9 183925	2	AC078870	AC078870 Homo sapi
c 740	19	2.9 175306	9	AC079948	AC079948 Homo sapi	c 797	19	2.9 183982	2	AC009825	AC009825 Homo sapi
c 741	19	2.9 175382	9	AL157836	AL157836 Human DNA	c 798	19	2.9 184137	9	AP005625	AP005625 Homo sapi
c 742	19	2.9 175549	10	AC126244	AC126244 Mus muscu	c 799	19	2.9 184155	10	AC124460	AC124460 Mus muscu
c 743	19	2.9 175775	9	AC112197	AC112197 Homo sapi	c 800	19	2.9 184214	9	AC145782	AC145782 Homo sapi
c 744	19	2.9 175825	9	HS10618	Z97193 Human DNA s	c 801	19	2.9 184351	2	AC079783	AC079783 Homo sapi
c 745	19	2.9 175880	10	BX001068	BX001068 Mouse DNA	c 802	19	2.9 184736	10	AC121767	AC121767 Mus muscu
c 746	19	2.9 176268	9	BS000082	BS000082 Pan trogl	c 803	19	2.9 184870	9	AC117386	AC117386 Homo sapi
c 747	19	2.9 176318	2	AC146186	AC146186 Pan trogl	c 804	19	2.9 184896	2	AC113228	AC113228 Sus scrofa
c 748	19	2.9 176329	2	AC117968	AC117968 Rattus no	c 805	19	2.9 185775	10	AC121967	AC121967 Homo sapi
c 749	19	2.9 176518	9	AC023933	AC023933 Homo sapi	c 806	19	2.9 185850	9	AL157394	AL157394 Human DNA
c 750	19	2.9 176539	10	AC127366	AC127366 Mus muscu	c 807	19	2.9 185930	9	AC023051	AC023051 Homo sapi
c 751	19	2.9 176668	2	AC021096	AC021096 Homo sapi	c 808	19	2.9 186072	2	AC022372	AC022372 Homo sapi
c 752	19	2.9 176787	2	AC021374	AC021374 Homo sapi	c 809	19	2.9 186078	9	AC090985	AC090985 Homo sapi
c 753	19	2.9 176947	9	HS170A21	Z82189 Human DNA s	c 810	19	2.9 186110	2	AC102204	AC102204 Mus muscu
c 754	19	2.9 176995	2	BX323050	BX323050 Dantio rer	c 811	19	2.9 186167	2	AC145618	AC145618 Homo sapi
c 755	19	2.9 177041	2	AC026344	AC026344 Homo sapi	c 812	19	2.9 186183	9	AC079857	AC079857 Homo sapi
c 756	19	2.9 177180	9	HS47384	Z83928 Human DNA s	c 813	19	2.9 186219	9	AC079857	AC079857 Homo sapi
c 757	19	2.9 177231	2	AC073259	AC073259 Homo sapi	c 814	19	2.9 186359	2	AC111041	AC111041 Homo sapi
c 758	19	2.9 177428	5	AL840641	AL840641 Zebrafish	c 815	19	2.9 186544	2	BX649638	BX649638 Dantio rer
c 759	19	2.9 177585	9	AC005826	AC005826 Homo sapi	c 816	19	2.9 186687	9	AC010744	AC010744 Homo sapi
c 760	19	2.9 177656	9	AL390783	AL390783 Human DNA	c 817	19	2.9 186693	2	AC013504	AC013504 Homo sapi
c 761	19	2.9 177728	2	AP001358	AP001358 Homo sapi	c 818	19	2.9 186836	9	AC079340	AC079340 Homo sapi
c 762	19	2.9 177873	2	AC122486	AC122486 Mus muscu	c 819	19	2.9 186930	2	AC135873	AC135873 Homo sapi
c 763	19	2.9 177921	2	AC112343	AC112343 Rattus no	c 820	19	2.9 187121	10	AC127290	AC127290 Mus muscu
c 764	19	2.9 178610	5	BX324159	BX324159 Zebrafish	c 821	19	2.9 187296	2	AC146229	AC146229 Homo sapi
c 765	19	2.9 178660	9	AC009852	AC009852 Homo sapi	c 822	19	2.9 187306	9	AC069226	AC069226 Homo sapi
c 766	19	2.9 178664	2	BX511115	BX511115 Dantio rer	c 823	19	2.9 187316	9	AL139340	AL139340 Human DNA
c 767	19	2.9 178804	2	AC016918	AC016918 Homo sapi	c 824	19	2.9 187585	2	BX539348	BX539348 Homo sapi
c 768	19	2.9 179098	9	AC092650	AC092650 Homo sapi	c 825	19	2.9 187651	2	AC055122	AC055122 Homo sapi
c 769	19	2.9 179194	2	AC146925	AC146925 Homo sapi	c 826	19	2.9 187778	2	AC027180	AC027180 Homo sapi
c 770	19	2.9 179461	2	AC019177	AC019177 Homo sapi	c 827	19	2.9 188048	10	AL669974	AL669974 Homo sapi
c 771	19	2.9 180035	2	AC125819	AC125819 Rattus no	c 828	19	2.9 188104	2	AC094551	AC094551 Homo sapi
c 772	19	2.9 180140	2	AC145521	AC145521 Papio ham	c 829	19	2.9 188515	2	AC102531	AC102531 Mus muscu
c 773	19	2.9 180347	9	AC009415	AC009415 Homo sapi	c 830	19	2.9 188527	9	AC084357	AC084357 Homo sapi
c 774	19	2.9 180401	9	AC007489	AC007489 Homo sapi	c 831	19	2.9 188527	9	AC084357	AC084357 Homo sapi

832	19	2.9	188754	2	BX005169	BX005169 Dantlo rer	889	19	2.9	203715	2	AC018807	AC018807 Homo sapi
833	19	2.9	188787	2	AC090215	AC090215 Homo sapi	890	19	2.9	203841	2	AC141954	AC141954 Rattus no
834	19	2.9	188903	2	AC143524	AC143524 Papilo ham	891	19	2.9	204125	2	BX005025	BX005025 Dantlo rer
835	19	2.9	188914	9	AC019118	AC019118 Homo sapi	892	19	2.9	204158	2	AC127194	AC127194 Rattus no
836	19	2.9	189018	9	AC091185	AC091185 Homo sapi	893	19	2.9	204662	9	CNS01RHO	AL162191 Human chr
837	19	2.9	189036	2	AC019142	AC019142 Homo sapi	894	19	2.9	205825	9	AC146011	AC146011 Pan trogl
838	19	2.9	189062	2	AP001106	AP001106 Homo sapi	895	19	2.9	206093	2	BX571844	BX571844 Dantlo rer
839	19	2.9	189559	9	AC099845	AC099845 Homo sapi	896	19	2.9	206322	2	AC108891	AC108891 Bos tauru
840	19	2.9	189758	2	AC115807	AC115807 Mus muscu	897	19	2.9	206358	2	AC142250	AC142250 Mus muscu
841	19	2.9	189819	2	AP002475	AP002475 Homo sapi	898	19	2.9	207124	2	AC119648	AC119648 Rattus no
842	19	2.9	189876	2	AC084810	AC084810 Homo sapi	899	19	2.9	207362	2	AC119648	AC119648 Rattus no
843	19	2.9	189893	2	AC013254	AC013254 Drosophi1	900	19	2.9	207582	2	AC144674	AC144674 Rattus no
844	19	2.9	190012	2	BX629351	BX629351 Dantlo rer	901	19	2.9	207840	5	BX005008	BX005008 Zebrafish
845	19	2.9	190015	9	AC087639	AC087639 Homo sapi	902	19	2.9	207842	9	AC010276	AC010276 Homo sapi
846	19	2.9	190096	2	BX119962	BX119962 Dantlo rer	903	19	2.9	209384	2	AC016818	AC016818 Homo sapi
847	19	2.9	190168	2	BX088561	BX088561 Dantlo rer	904	19	2.9	210189	10	AC123074	AC123074 Mus muscu
848	19	2.9	190325	3	AC007904	AC007904 Drosophi1	905	19	2.9	210949	2	AC146885	AC146885 Gallitlthrl
849	19	2.9	190801	3	AC009212	AC009212 Drosophi1	906	19	2.9	211331	5	BX511214	BX511214 Zebrafish
850	19	2.9	190961	9	AC007458	AC007458 Homo sapi	907	19	2.9	211571	5	BX248124	BX248124 Zebrafish
851	19	2.9	191017	2	AC034286	AC034286 Mus muscu	908	19	2.9	211934	10	AL777223	AL777223 Mouse DNA
852	19	2.9	191133	9	AC142213	AC142213 Pan trogl	909	19	2.9	212670	2	AC120420	AC120420 Mus muscu
853	19	2.9	191197	2	AP001779	AP001779 Homo sapi	910	19	2.9	212873	2	AC139521	AC139521 Rattus no
854	19	2.9	191655	2	AC110267	AC110267 Mus muscu	911	19	2.9	213150	2	AC107642	AC107642 Mus muscu
855	19	2.9	192003	10	AC084292	AC084292 Mus muscu	912	19	2.9	213625	2	AC102114	AC102114 Mus muscu
856	19	2.9	192048	2	AC141574	AC141574 Rattus no	913	19	2.9	213740	9	AC004980	AC004980 Homo sapi
857	19	2.9	193600	5	AL929261	AL929261 Zebrafish	914	19	2.9	213934	2	BX293565	BX293565 Dantlo rer
858	19	2.9	194240	9	AC144378	AC144378 Pan trogl	915	19	2.9	214082	2	AL928848	AL928848 Dantlo rer
859	19	2.9	194247	9	AC128060	AC128060 Rattus no	916	19	2.9	214643	2	AC136848	AC136848 Rattus no
860	19	2.9	194543	2	AC027630	AC027630 Homo sapi	917	19	2.9	214799	10	AL833798	AL833798 Mouse DNA
861	19	2.9	194702	9	AC024198	AC024198 Homo sapi	918	19	2.9	214843	5	BX005203	BX005203 Zebrafish
862	19	2.9	194813	2	AC100723	AC100723 Mus muscu	919	19	2.9	215898	2	AC096428	AC096428 Rattus no
863	19	2.9	194924	10	AC126250	AC126250 Mus muscu	920	19	2.9	216302	2	AC107116	AC107116 Rattus no
864	19	2.9	195064	2	AC110271	AC110271 Mus muscu	921	19	2.9	216877	2	AC121293	AC121293 Mus muscu
865	19	2.9	195813	10	AC068912	AC068912 Mus muscu	922	19	2.9	217000	2	AC114158	AC114158 Rattus no
866	19	2.9	195942	2	AC117672	AC117672 Mus muscu	923	19	2.9	217743	2	AC115704	AC115704 Mus muscu
867	19	2.9	196175	10	AC069019	AC069019 Mus muscu	924	19	2.9	218097	2	AC134071	AC134071 Rattus no
868	19	2.9	196923	10	AC108948	AC108948 Mus muscu	925	19	2.9	218105	2	AC108831	AC108831 Mus muscu
869	19	2.9	197828	2	AC034169	AC034169 Homo sapi	926	19	2.9	218347	2	AC126889	AC126889 Rattus no
870	19	2.9	198401	2	AC107803	AC107803 Mus muscu	927	19	2.9	218558	2	AC025964	AC025964 Mus muscu
871	19	2.9	198463	10	AC123038	AC123038 Mus muscu	928	19	2.9	218597	5	BX537113	BX537113 Zebrafish
872	19	2.9	198470	9	AC046170	AC046170 Homo sapi	929	19	2.9	219340	10	AL670771	AL670771 Mouse DNA
873	19	2.9	199493	10	AC122271	AC122271 Mus muscu	930	19	2.9	219550	2	AC135904	AC135904 Rattus no
874	19	2.9	199893	2	AC025529	AC025529 Mus muscu	931	19	2.9	219792	2	AC100244	AC100244 Mus muscu
875	19	2.9	200395	9	AF274855	AF274855 Homo sapi	932	19	2.9	220189	2	AC109406	AC109406 Rattus no
876	19	2.9	200620	9	AC138645	AC138645 Homo sapi	933	19	2.9	220414	2	BX546482	BX546482 Dantlo rer
877	19	2.9	200677	9	AC090079	AC090079 Homo sapi	934	19	2.9	220903	2	AC126005	AC126005 Rattus no
878	19	2.9	200939	2	BX548248	BX548248 Dantlo rer	935	19	2.9	221190	2	BX571704	BX571704 Dantlo rer
879	19	2.9	200721	2	AC119742	AC119742 Homo sapi	936	19	2.9	221568	2	AC103452	AC103452 Rattus no
880	19	2.9	200853	2	AC132988	AC132988 Rattus no	937	19	2.9	221981	2	AC103165	AC103165 Rattus no
881	19	2.9	201902	5	BX004822	BX004822 Zebrafish	938	19	2.9	222384	2	AC121111	AC121111 Mus muscu
882	19	2.9	202012	5	BX088583	BX088583 Zebrafish	939	19	2.9	222593	10	AC124360	AC124360 Mus muscu
883	19	2.9	202342	10	AL583884	AL583884 Mouse DNA	940	19	2.9	222918	2	AC111433	AC111433 Rattus no
884	19	2.9	202653	9	AC026682	AC026682 Mus muscu	941	19	2.9	223283	9	AC146172	AC146172 Pan trogl
885	19	2.9	202719	9	AC006379	AC006379 Homo sapi	942	19	2.9	223385	2	BX248513	BX248513 Dantlo rer
886	19	2.9	202777	5	BX005020	BX005020 Zebrafish	943	19	2.9	223785	2	AC103310	AC103310 Rattus no
887	19	2.9	202842	10	AL607108	AL607108 Mouse DNA	944	19	2.9	223940	2	AC087567	AC087567 Mus muscu
888	19	2.9	203714	2	AC141903	AC141903 Rattus no	945	19	2.9	223948	3	AE003703	AE003703 Drosophi1

ALIGNMENTS			
RESULT 1			
BD245276	651 bp	DNA	Linear PAT 17-JUL-2003
LOCUS			
DEFINITION	BD245276	Development of novel antibiotics based on bacteriophage genomics.	
ACCESSION	BD245276.1	GI:33055046	
VERSION	JP 2002531107-A/11.		
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 651)		
AUTHORS	Pelletier,J., Gros,P. and Dubow,M.		
TITLE	Development of novel antibiotics based on bacteriophage genomics		
JOURNAL	Patent: JP 2002531107-A 11 24-SEP-2002;		
COMMENT	PHAGETECH INC		
OS	Staphylococcus aureus bacteriophage 77		
PN	JP 2002531107-A/11		
PD	24-SEP-2002		
PR	03-DEC-1999 JP 2000585456		
PF	03-DEC-1999 US 60/110992, 03-JUN-1999 US 09/326144 PR		
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR			
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PELLETIER, PHILIPPE GROS, MICHAEL DUBOW			
PC	CI2N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,		
PC	CI2M1/00,		
PC	CI2N15/21, CI2Q1/02, CI2Q1/68, G01N33/15, G01N33/50, G01N33/566, PC		
CI2N15/00			
PC	A61K37/02		
CC	Coding Sequence		
EH	Key	Location/Qualifiers	
FT	source	1..651	
FT	aureus bacteriophage 77'	/organism='Staphylococcus	
FEATURES			
source	Location/Qualifiers		
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	/organism='unidentified'		
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ORIGIN			
Query Match	100.0%; Score 651; DB 6; Length 651;		
Best Local Similarity	100.0%; Pred. No. 2, 3e-285;		
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ATGAACGACGAAATATATGGAAGCATATATACCTTACAGGAGGTGTGCTTATATCA 60		
DB	1 ATGAACGACGAAATATATGGAAGCATATATACCTTACAGGAGGTGTGCTTATATCA 60		
QY	61 GTTAAAGATTTTATAGATTTTATTCAGATCTCAACTCAACGTAATAAAATCATTTA 120		
DB	61 GTTAAAGATTTTATAGATTTTATTCAGATCTCAACTCAACGTAATAAAATCATTTA 120		
QY	121 GAACAAATATATCGATATATTTAGATGTTTAAAAAGGCTAAAAAGATGATGGAGCT 180		

Db 121 GACAAATATATCGATATATTTAGATTTGTTAAAAAGGTAAAAAGATATGAGCT 180
 Oy 181 TATATTATTCAGACGACGATGATTTTATGATTTTATGATGAGCTTAT 240
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 Oy 361 AGTCAAAATGATTTTATTCCTTTTGTATGAAACATGCTATATAT 420
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 Oy 421 GATATCAAAAAGATATATCTATTTAAAAATATTAATTAATGATGAAATGAC 480
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 Oy 541 AATCTTATCTGATTAATTTAGACAGCTTTAGTAAATGATTAACAGACT 600
 Db 541 AATCTTATCTGATTAATTTAGACAGCTTTAGTAAATGATTAACAGACT 600
 Oy 601 TCGATTAAGAAAGATATATTTAATTTAAAGAGAGAGATTTAAATGA 651
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RESULT 2
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 LOCUS Bacteriophage phi PVL proviral DNA, complete sequence.
 DEFINITION AB009866
 ACCESSION AB009866.2 GI:8051688
 VERSION
 KEYWORDS integrase; LukE-PV; LukS-PV; holin; amidase (peptidoglycan hydrolase); capsid protein; portal protein.
 SOURCE
 ORGANISM
 Staphylococcus aureus bacteriophage PVL
 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 REFERENCE
 1 (sites)
 Kaneko, J., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
 Pantone-valentine leukocidin genes in a phage-like particle isolated from mitecycin C-treated *Staphylococcus aureus* V8 (ATCC 49775)
 JOURNAL
 Biochem. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
 MEDLINE
 98067870
 PUBMED
 9404084
 2 (sites)
 Kaneko, J., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.

TITLE Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPVL carrying Pantone-Valentine leukocidin genes
 JOURNAL Gene 215 (1), 57-67 (1998)
 MEDLINE 98332719
 PUBMED 9666077
 REFERENCE 3 (bases 1 to 41401)
 AUTHORS Kaneko, J., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.
 TITLE Direct Submision
 JOURNAL Biol. Chem., Faculty of Agriculture, 1-1 Tsutsumi-dori Aomiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan (E-mail: jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781, Fax:81-22-717-8780)
 COMMENT On May 24, 2000 this sequence version replaced gi:3341907.
 Sequence updated (06-Feb-1998)
 Sequence updated (22-May-2000).
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 537..2231
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KREMDLQKYSIDQINGLSLDTLSRTIESDNGDFLNFNLNGTGHGGLLQKQV
LNKAKADNAREEFHKSFSGTQKGVVYLDSEKTDQLEVDTEKLIRNKSSTRE
IAGVFGIPLHKEIGETANNSTIDANLDYLSLAKPYITCVCAELNFENDEYVNEFE
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/db_xref="GI:3341914"

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/codon_start=1
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DYVEFQNDVEQNFIDRLPESSHVITGYDKKSGTGRDYVMEFTFKTYDEFNSRGE
QYMEPVYKEMKRTKEVNTSVNVTDEQVTKVDATKOLSAITPEPSQNVYVATBEOQ
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Best Local Similarity	100.0%;	Pred. No. 1.3e-285;		
Matches 651;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Db	39659	TCGATAAAGAAAGATTTATTTATTTAAACAAAGGAGATTAAATGA	39709
RESULT 3			
LOCUS	BD245281	41708 bp	DNA
DEFINITION	Development of novel antibiotics based on bacteriophage	linear	PAT 17-JUL-2003
ACCESSION	BD245281	GI:33055051	genomics.
VERSION	BD245281.1	GI:33055051	
KEYWORDS	JP 2002531107-A/16.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 41708)		
AUTHORS	Pelletier,J., Gros,P., and Dubow,M.		
TITLE	Development of novel antibiotics based on bacteriophage		
JOURNAL	Patent: JP 2002531107-A 16 24-SEP-2002;		
COMMENT	PHAGETECH INC		
	OS Staphylococcus aureus bacteriophage 77		
	PN JP 2002531107-A/16		
	PD 24-SEP-2002		
	PF 03-DEC-1999 JP 2000585456		
	PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR		
	28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR		
	01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 P1		JERBY
	PELLETIER, PHILIPPE GROS, MICHAEL DUBOW		
	PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,		
	PC C12M1/00,		
	PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC		
	C12N15/00,		
	PC A61K37/02		
	CC Genome Sequence		
	FM Key	Location/Qualifiers	
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	FT	/organism="Staphylococcus	
	aureus bacteriophage	771.	
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Query Match	100.0%; Score 651; DB 6; Length 41708;		
Best Local Similarity	100.0%; Pred. No. 1.3e-285;		
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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OY	61 GTTAAAGACATTTTGGATTTTACGATCTCACTCACTTCAACAGTAAAAAATCAATTTA 120		
DB	39911 GTTAAAGACATTTTGGATTTTACGATCTCACTCACTTCAACAGTAAAAAATCAATTTA 39970		

QY 121 GACAAATATATCCGATATATTTAGATTGTTTAAAAAGCTAAAAAGATGATGAGCT 180
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Db 39971 GACAAATATATCCGATATATTTAGATTGTTTAAAAAGCTAAAAAGATGATGAGCT 40030
QY 181 TATATTATTCACAGACAGACATGATTTTATGATTTTATGATGAGCTTTAT 240
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Db 40031 TATATTATTCACAGACAGACATGATTTTATGATTTTATGATGAGCTTTAT 40090
QY 241 AATTAGATACGAAAGTAAAAAGCTATGAAAATGTTATTGGATTAGCAAAATGAT 300
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Db 40091 AATTAGATACGAAAGTAAAAAGCTATGAAAATGTTATTGGATTAGCAAAATGAT 40150
QY 301 AATTATCAAAATAGATTAGGCAATGGAAGATTTTAAAGATGATTTCAACATGATTT 360
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Db 40151 AATTATCAAAATAGATTAGGCAATGGAAGATTTTAAAGATGATTTCAACATGATTT 40210
QY 361 AGTACAAATCAGATTTTATATCTCTTTGTTATGAAACATGCTATTATTAAT 420
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Db 40211 AGTACAAATCAGATTTTATATCTCTTTGTTATGAAACATGCTATTATTAAT 40270
QY 421 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATTAATGAATGAAATAGA 480
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Db 40271 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATTAATGAATGAAATAGA 40330
QY 481 GCTTATATCATATGATAGTTTATCTCTCTGATCAGATACGAGAAAATTAACGATAT 540
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Db 40331 GCTTATATCATATGATAGTTTATCTCTCTGATCAGATACGAGAAAATTAACGATAT 40390
QY 541 AATCTTATCTTGATTAATTTGAGACAGCTTTAGTCAAAAGTTTAAATTAACAGAT 600
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QY 601 TCGATAAAAAGAAATATATTTATTTAAACAAGAGATTTAAATGA 651
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Db 40451 TCGATAAAAAGAAATATATTTATTTAAACAAGAGATTTAAATGA 40501

RESULT 4
AR368770 AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS
DEFINITION Sequence 3 from patent US 637652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,D., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential *Staphylococcus aureus* gene and its encoded protein
JOURNAL Patent: US 637652-A 3 23-APR-2002;
FEATURES
1..41708
Location/Qualifiers
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 651; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 1.3e-285;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 39911 GTTAAAGATTTTATGATTTTACAGATTTTACACTTACACAGTAAATTAATTTCA 39970
QY 121 GACAAATATATCCGATATATTTAGATTGTTTAAAAAGCTAAAAAGATGATGAGCT 180
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Db 39971 GACAAATATATCCGATATATTTAGATTGTTTAAAAAGCTAAAAAGATGATGAGCT 40030
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Db 40151 AATTATCAAAATAGATTAGGCAATGGAAGATTTTAAAGATGATTTCAACATGATTT 40210
QY 361 AGTACAAATCAGATTTTATATCTCTTTGTTATGAAACATGCTATTATTAAT 420
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QY 421 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATTAATGAATGAAATAGA 480
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Db 40331 GCTTATATCATATGATAGTTTATCTCTCTGATCAGATACGAGAAAATTAACGATAT 40390
QY 541 AATCTTATCTTGATTAATTTGAGACAGCTTTAGTCAAAAGTTTAAATTAACAGAT 600
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Db 40391 AATCTTATCTTGATTAATTTGAGACAGCTTTAGTCAAAAGTTTAAATTAACAGAT 40450
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Db 40451 TCGATAAAAAGAAATATATTTATTTAAACAAGAGATTTAAATGA 40501

RESULT 5
AP004828/c AP004828 272850 bp DNA linear BCT 20-DEC-2002
LOCUS
DEFINITION *Staphylococcus aureus* subsp. *aureus* NM2 DNA, complete genome,
strain:NM2, section 7/10.
ACCESSION AP004828 BA000033
VERSION AP004828.1 GI:21204850

Db 249706 AATTATCAATAGATTAAAGCAATGAAATTTTAAAGATGAGTTCAAGATGATTT
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 249646 AGTACAAATCAGATTTTATTCCTTTTGTATGAAACATGCTATTATAT
 249637
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 249586 GAATATCAAAAGATATATCTATTATTTAAATATATTAATTAATGAATGAATGA
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 249526 GCTATATCATATGATGATGATTTATCATCTTACAGTACGACGAAATTAACGATTT
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 Qy 541 AATCTTATCTGATTAATTTGAAGACGTTTACTGAAAGTTTAAATTAACGACT 600
 249466 AATCTTATCTGATTAATTTGAAGACGTTTACTGAAAGTTTAAATTAACGACT
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 249406 TCGATTAAGAAAGATTTATTTATTTAAACAGAGAGATTTAATGA 249356
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 RESULT 6
 AC130112 236256 bp DNA linear HTG 13-MAY-2003
 LOCUS Rattus norvegicus clone CH230-100B18, WORKING DRAFT SEQUENCE, 3
 DEFINITION
 UNORDERED PIECES.
 AC130112
 AC130112.3 GI:30579729
 VERSION HTG, HTGS, PHASE1; HTGS, DRAFT; HTGS, FULLTOP.
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 236256)
 Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Albrooks, S., Amin, A., Angilano, D.,
 Anyaloboch, V., Aoyagi, A., Ayodeji, H., Baca, B., Baden, H.,
 Baldwin, D., Bandarenko, D., Barber, M., Barnstead, M., Benedek, F.,
 Bismah, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Burch, K., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Cantler, A.,
 Chavel, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carrroll, L., De Andrade, C., Dedrich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., DiVito, K.,
 Drepper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,
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 Frazer, C. M., Gabisi, A., Gante, R., Garcia, A., Garner, T., Garza, M.,

Georgiev, E., Geor, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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 Kowalski, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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 Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Muddusa, M., Murphy, K., Nair, L.,
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 Puzo, M., Qutob, J., Rachlin, E., Reeves, K., Reigh, M., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
 Shorty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smales, D.,
 Smedley, A., Sodergren, E., Song, X., Z., Sotelle, R., Soza, J.,
 Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, J., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,
 Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wolozky, R., Woodson, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, O., Yoon, Y., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstein, G., and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 236256)
 Worley, K. C.
 Direct Submission
 Submitted (08-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 236256)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 13, 2003 this sequence version replaced gi:22855970.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GJFJ

Center clone name: CH230-100B18

----- Summary Statistics

Assembly program: Atlas 3.0j

Consensus quality: 224059 bases at least Q40

Consensus quality: 225273 bases at least Q30

Consensus quality: 226227 bases at least Q20

Estimated insert size: 233388; sum-of-contigs estimation

Quality coverage: 10x in Q20 bases; sum-of-contigs estimation

- * NOTE: Estimated insert size may differ from sequence length
- * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 3 contigs. The true order of the pieces
- * is not known and their order in this sequence record is
- * arbitrary. Gaps between the contigs are represented as
- * runs of N, but the exact sizes of the gaps are unknown.
- * This record will be updated with the finished sequence
- * as soon as it is available and the accession number will
- * be preserved.

- * 1 233677: contig of 233677 bp in length
- * 233678 233777: gap of unknown length
- * 233778 234933: contig of 1156 bp in length
- * 234934 235033: gap of unknown length
- * 235034 236256: contig of 1223 bp in length.

FEATURES

source

1..236256
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-100B18"

ORIGIN

Query Match 3.8% Score 25; DB 2; Length 236256;
Best Local Similarity 100.0%; Fred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TATTAGATTGTTTAAAAAGGCTA 163
|||||

DB 225301 TATTAGATTGTTTAAAAAGGCTA 225325

Search completed: October 15, 2004, 03:29:20
Job time: 3418.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 18:55:29 ; Search time 434.29 Seconds
(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-804A-5

Perfect score: 651
Sequence: 1 atgaacgagcaataatagg.....acaagagagatuaatga 651

Scoring table:
Gapop 60.0, Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: N_Geneseq_29Jan04.*

- 1: geneseqn180s.*
- 2: geneseqn190s.*
- 3: geneseqn200s.*
- 4: geneseqn201s.*
- 5: geneseqn2001s.*
- 6: geneseqn2002s.*
- 7: geneseqn2003s.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	651	3 AAA68249	Aa68249 Bacterioph
2	651	100.0	41708	3 AAA68247	Aa68247 Bacterioph
3	651	100.0	41708	4 AAC86106	Aac86106 Complete
4	23	3.5	305	3 AAC94532	Aac94532 Cat file
5	22	3.4	4007	4 AAL06007	Aa106007 Human rep
6	22	3.4	4007	4 AB198572	Ab198572 Human tes
7	22	3.4	13449	6 AB133384	Ab133384 Human imm

c	8	21	3.2	438	3	AA56843	AA56843 Mycoplasma
c	9	21	3.2	33665	4	ABU08422	AbU08422 Drosophila
c	10	21	3.2	66743	4	ABL27118	AbL27118 Drosophila
c	11	20	3.1	98	2	AA25626	AA25626 Human gen
c	12	20	3.1	454	6	ABL69046	AbL69046 Kidney ca
c	13	20	3.1	492	3	AA56954	AA56954 Human col
c	14	20	3.1	492	6	ABT12376	AbT12376 Oocytes a
c	15	20	3.1	492	6	ACD91670	AcD91670 Human col
c	16	20	3.1	835	6	ABQ46604	AbQ46604 Oligonuc
c	17	20	3.1	835	6	ABQ46605	AbQ46605 Oligonuc
c	18	20	3.1	887	6	ABQ48892	AbQ48892 Oligonuc
c	19	20	3.1	887	6	ABQ48893	AbQ48893 Oligonuc
c	20	20	3.1	1008	7	ACA24386	AcA24386 Prokaryot
c	21	20	3.1	1206	6	ABQ21670	AbQ21670 Oligonuc
c	22	20	3.1	1206	6	ABQ21671	AbQ21671 Oligonuc
c	23	20	3.1	1232	6	ABQ17902	AbQ17902 Oligonuc
c	24	20	3.1	1232	6	ABQ17903	AbQ17903 Oligonuc
c	25	20	3.1	1323	7	ACA47835	AcA47835 Prokaryot
c	26	20	3.1	1505	2	AA399568	AA399568 Nucleic a
c	27	20	3.1	1594	6	ABT10839	AbT10839 Human bre
c	28	20	3.1	4836	4	ABU08818	AbU08818 Drosophila
c	29	20	3.1	5454	3	AA470189	AA470189 Plasmodu
c	30	20	3.1	6775	6	ABQ67159	AbQ67159 Human ang
c	31	20	3.1	10194	4	ABU08154	AbU08154 Drosophila
c	32	20	3.1	10855	6	ABU33489	AbU33489 Human imm
c	33	20	3.1	14335	4	AAE28824	AAE28824 Genomic f
c	34	20	3.1	14766	4	ABU05848	AbU05848 Drosophila
c	35	20	3.1	18585	6	ABU34608	AbU34608 Human met
c	36	19	2.9	190	4	ABK41908	AbK41908 cDNA enco
c	37	19	2.9	190	8	ADB59575	ADb59575 Connectiv
c	38	19	2.9	303	4	ABK42649	ABk42649 Genomic s
c	39	19	2.9	303	8	ADB60805	ADb60805 Connectiv
c	40	19	2.9	357	4	ABK08757	ABk08757 Human sec
c	41	19	2.9	362	5	ABV15180	ABv15180 Human pro
c	42	19	2.9	471	6	AB217006	AB217006 Arabidops
c	43	19	2.9	532	3	AA53493	AA53493 Arabidops
c	44	19	2.9	753	4	AAH70213	AAh70213 Human cer
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c	47	19	2.9	1015	6	ABQ43983	AbQ43983 Oligonuc
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c	50	19	2.9	2903	4	ABU26074	AbU26074 Drosophila
c	51	19	2.9	3345	4	ABU14304	AbU14304 Drosophila
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c	53	19	2.9	6061	6	ABU32141	AbU32141 Human imm
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c	66	19	2.9	17934	6	ABU33719	ABu33719 Human imm
c	67	19	2.9	18817	6	ABU34494	ABu34494 Human met
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c	72	19	2.9	110000	8	ACH03408	ACH03408 Continuation (2 of
c	73	19	2.9	133894	2	AA113635	AA113635 AcNFV gen
c	74	19	2.9	269223	4	AAE28554	AAE28554 Genomic f
c	75	19	2.9	335913	5	AA161371	AA161371 Soybean 2
c	76	19	2.9	335913	5	AA161372	AA161372 Soybean 2
c	77	18	2.8	148	2	AAH87023	AAh87023 Human sin
c	78	18	2.8	229	2	AAH11511	AAh11511 Human b1a
c	79	18	2.8	301	3	AAE61543	AAE61543 Rearrange
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c	81	18	2.8	323	6	ABK91810	ABk91810 DNA enco
c	82	18	2.8	333	6	ABQ67409	ABq67409 Listeria
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c	84	18	2.8	355	9	ADE51549	ADe51549 D EGF rec
c	85	18	2.8	376	6	ABK91824	ABk91824 DNA enco
c	86	18	2.8	379	4	AAK56124	AAK56124 Human imm
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c	88	18	2.8	423	4	AAH53235	AAh53235 S. epider
c	89	18	2.8	444	8	ACH24147	ACH24147 Human adu
c	90	18	2.8	459	7	ABK42501	ABk42501 Bovine ES
c	91	18	2.8	474	4	AAH34212	AAh34212 Human col
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c	105	18	2.8	1141	6	ABQ34257	ABq34257 Oligonuc
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c	107	18	2.8	1164	7	ACH27492	ACH27492 Truncated
c	108	18	2.8	1167	6	ABN91484	ABn91484 Staphyloc
c	109	18	2.8	1230	7	ACCT2028	ACc22028 BCU0475 g
c	110	18	2.8	1809	6	AB215899	AB215899 Arabidops
c	111	18	2.8	1821	6	ABD29066	ABd29066 Phaeo
c	112	18	2.8	1832	6	ABN83929	ABn83929 Truncated
c	113	18	2.8	2352	6	ABE32123	ABe32123 Caridida a
c	114	18	2.8	3041	9	AAH66944	AAH66944 C. neofo
c	115	18	2.8	3076	4	AAH54938	AAH54938 S. epider
c	116	18	2.8	3165	9	ADB62426	ADB62426 Human cDN
c	117	18	2.8	3529	4	ABU30510	ABU30510 Drosophila
c	118	18	2.8	3555	4	AAH54844	AAH54844 S. epider
c	119	18	2.8	3578	4	ABU30502	ABU30502 Drosophila
c	120	18	2.8	3827	4	ABU24964	ABU24964 Drosophila
c	121	18	2.8	3863	4	ABU06242	ABU06242 Drosophila

122	18	2.8	4138	AAH54631	Abi54631 S. opider	179	18	2.8	13537	4	AAK68964	AAK68964 Human imm
123	18	2.8	4413	ABU04492	AbU04492 Drosophila	180	18	2.8	14551	6	ABJ34585	AbJ34585 Human met
124	18	2.8	4670	AAK67409	AAK67409 Human imm	c 181	18	2.8	15161	6	ABU70458	ABU70458 Chemical
125	18	2.8	4670	AAK67410	AAK67410 Human imm	c 182	18	2.8	15161	6	AA561423	AA561423 Human gen
c 126	18	2.8	5326	ABU29736	ABU29736 Drosophila	183	18	2.8	15853	6	ABU70466	ABU70466 Chemical
c 127	18	2.8	5702	AD663604	AD663604 Rat gene	184	18	2.8	15853	6	AA561457	AA561457 Human gen
c 128	18	2.8	5702	AD663603	AD663603 Rat gene	185	18	2.8	16258	6	ABK40037	ABK40037 Human che
c 129	18	2.8	5702	AD663605	AD663605 Rat gene	186	18	2.8	16258	6	ABU70375	ABU70375 Chemical
c 130	18	2.8	5702	AA545426	AA545426 Chemical	c 187	18	2.8	17137	6	ABJ32190	ABJ32190 Human imm
c 131	18	2.8	6012	ABJ34059	ABJ34059 Human imm	c 188	18	2.8	18011	6	ABJ32035	ABJ32035 Human imm
c 132	18	2.8	6012	ABJ34059	ABJ34059 Human imm	189	18	2.8	18060	6	ABU92212	ABU92212 Chemical
c 133	18	2.8	6020	ABJ32199	ABJ32199 Human imm	190	18	2.8	18060	6	AAU22313	AAU22313 Chemical
c 134	18	2.8	6020	ABJ32199	ABJ32199 Human imm	c 191	18	2.8	18624	6	ABJ33703	ABJ33703 Human imm
c 135	18	2.8	6149	AA563307	AA563307 Chemical	c 192	18	2.8	19131	4	AA546717	AA546717 Tumour su
c 136	18	2.8	6167	ABK31406	ABK31406 Signal tr	c 193	18	2.8	20268	4	AAK90183	AAK90183 Human dig
c 137	18	2.8	6167	ABU70367	ABU70367 Chemical	c 194	18	2.8	20268	4	AAI57636	AAI57636 Human col
c 138	18	2.8	6167	AA561329	AA561329 Human gen	c 195	18	2.8	20268	6	AB599813	AB599813 Genomic D
c 139	18	2.8	6175	AAU28373	AAU28373 Human che	c 196	18	2.8	20268	9	ABR92966	ABR92966 Human col
c 140	18	2.8	6204	AA545482	AA545482 Chemical	197	18	2.8	33053	6	ABQ67005	ABQ67005 Human ang
c 141	18	2.8	6204	ABJ34003	ABJ34003 Human imm	c 198	18	2.8	34488	5	AA597854	AA597854 Human neu
c 142	18	2.8	6204	ABK31477	ABK31477 Signal tr	c 199	18	2.8	34688	5	ABQ67059	ABQ67059 Human ang
c 143	18	2.8	6204	ABK28406	ABK28406 DNA trans	c 200	18	2.8	46852	7	ABQ76676	ABQ76676 Human ang
c 144	18	2.8	6204	ABN80267	ABN80267 Human che	c 201	18	2.8	46852	8	ADA02603	ADA02603 Mouse 112
c 145	18	2.8	6254	ABJ33621	ABJ33621 Human imm	c 202	18	2.8	65787	9	ABR72341	ABR72341 Mouse 112
c 146	18	2.8	6359	ABK39944	ABK39944 Human che	c 203	18	2.8	65787	9	ADA02675	ADA02675 Mouse Top
c 147	18	2.8	6392	ABJ32684	ABJ32684 Human imm	204	18	2.8	96389	8	ADB72413	ADB72413 Mouse Top
c 148	18	2.8	6392	ABJ34506	ABJ34506 Human met	c 205	18	2.8	110000	2	AAU20248	AAU20248 02
c 149	18	2.8	6467	ABN80169	ABN80169 Human che	c 206	18	2.8	110000	6	ABX08336	ABX08336 14
c 150	18	2.8	6582	ABQ74268	ABQ74268 Human 670	c 207	18	2.8	110000	6	ABA90521	ABA90521 00
c 151	18	2.8	6582	ADQ37486	ADQ37486 Human tra	c 208	18	2.8	110000	6	ABA90521	ABA90521 05
c 152	18	2.8	6609	ABJ33302	ABJ33302 Human imm	c 209	18	2.8	110000	6	ABQ67196	ABQ67196 1
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c 155	18	2.8	6620	ABN80278	ABN80278 Human che	c 212	18	2.8	110000	7	ACF67367	ACF67367 00
c 156	18	2.8	6727	ABJ33297	ABJ33297 Human imm	c 213	18	2.8	110000	7	ACF67367	ACF67367 16
c 157	18	2.8	6759	ABJ32739	ABJ32739 Human imm	c 214	18	2.8	110000	7	ACF67367	ACF67367 16
c 158	18	2.8	6852	ABU70311	ABU70311 Chemical	c 215	18	2.8	121162	3	AA566548	AA566548 Human kin
c 159	18	2.8	6880	AA561249	AA561249 Human gen	216	18	2.8	129021	3	AA562296	AA562296 BAC conta
c 160	18	2.8	7060	ABJ32453	ABJ32453 Human imm	c 217	18	2.8	139904	6	ABK83562	ABK83562 Human cin
c 161	18	2.8	7060	ABJ32930	ABJ32930 Drosophila	c 218	18	2.8	160771	6	ABQ88179	ABQ88179 Human ost
c 162	18	2.8	7106	ABJ33478	ABJ33478 Human imm	c 219	18	2.8	210710	7	ACF65380	ACF65380 Photocarb
c 163	18	2.8	7165	ABJ32750	ABJ32750 Human imm	c 220	18	2.8	218336	7	ABQ76678	ABQ76678 Photocarb
c 164	18	2.8	7165	ABK31266	ABK31266 Signal tr	c 221	18	2.8	235033	2	AAV57926	AAV57926 Heredilar
c 165	18	2.8	7165	ABU70221	ABU70221 Chemical	c 222	18	2.8	235033	2	AAV57926	AAV57926 Heredilar
c 166	18	2.8	7242	AB565034	AB565034 Invertebr	c 223	18	2.8	20	6	AA596661	AA596661 Telomeras
c 167	18	2.8	7360	ABJ33223	ABJ33223 Human imm	c 224	18	2.8	177	8	ABK41754	ABK41754 CDNA enco
c 168	18	2.8	9468	AAV25602	AAV25602 Feline im	c 225	18	2.8	184	6	ABV97353	ABV97353 Human pan
c 169	18	2.8	9817	ABJ33368	ABJ33368 Human imm	c 226	18	2.8	228	2	AAV08292	AAV08292 Porcine f
c 170	18	2.8	9848	ABJ33798	ABJ33798 Human imm	c 227	18	2.8	257	7	AAU55534	AAU55534 Human col
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c 172	18	2.8	10552	ABK31426	ABK31426 Signal tr	c 229	18	2.8	276	7	AB241094	AB241094 N. gonorr
c 173	18	2.8	10552	ABU70387	ABU70387 Chemical	c 230	18	2.8	276	7	AC241608	AC241608 N. gonorr
c 174	18	2.8	10552	AA561339	AA561339 Human gen	c 231	18	2.8	276	7	AC241482	AC241482 Prokaryot
c 175	18	2.8	10856	ABJ32456	ABJ32456 Human imm	c 232	18	2.8	279	7	AC241482	AC241482 Prokaryot
c 176	18	2.8	12711	ABJ34525	ABJ34525 Human met	c 233	18	2.8	329	3	AAU07773	AAU07773 Prokaryot
c 177	18	2.8	12711	ABU70250	ABU70250 Chemical	c 234	18	2.8	360	7	ABX65094	ABX65094 Human sec
c 178	18	2.8	13294	AAK65255	AAK65255 Human imm	c 235	18	2.8	366	4	ABK42355	ABK42355 Genomic s

236	17	2.6	366	4	ABK42356	Abd442356 Genomic s	293	17	2.6	620	6	ABQ48337	Abq46337 Oligonuc
237	17	2.6	366	8	ADB60312	Adb60312 Connectiv	294	17	2.6	624	7	ACF69878	Acf69878 Phototrab
238	17	2.6	366	8	ADB60511	Adb60511 Connectiv	c 295	17	2.6	628	4	AAF44913	Aaf44913 Human bre
239	17	2.6	369	5	ABV07523	Abv07523 Human pro	c 296	17	2.6	657	6	ABQ33142	Abq33142 Oligonuc
240	17	2.6	377	7	ABS57760	Abs57760 Mouse ang	297	17	2.6	657	6	ABQ33143	Abq33143 Oligonuc
c 241	17	2.6	379	4	AAS28559	Aas28559 Genomic s	298	17	2.6	665	4	AAH33146	Aah33146 Human col
c 242	17	2.6	379	4	AAS28057	Aas28057 Novel cDN	c 299	17	2.6	680	6	ABQ23708	Abq23708 Oligonuc
243	17	2.6	380	7	ABK44170	Abk44170 Bovine ES	c 300	17	2.6	680	6	ABQ25709	Abq25709 Oligonuc
244	17	2.6	386	9	ADB51762	Adb51762 ToxAclyt-	c 301	17	2.6	689	7	ADA68705	Ada68705 Rice gene
c 245	17	2.6	386	9	ADB51718	Adb51718 Primary r	c 302	17	2.6	695	6	ABQ46540	Abq46540 Oligonuc
c 246	17	2.6	389	5	AAF64257	Aaf64257 Novel hum	c 303	17	2.6	695	6	ABQ53161	Abq53161 Oligonuc
247	17	2.6	395	5	AAF64574	Aaf64574 Novel hum	304	17	2.6	695	6	ABQ46541	Abq46541 Oligonuc
248	17	2.6	396	5	ABV10093	Abv10093 Human pro	305	17	2.6	695	6	ABQ53160	Abq53160 Oligonuc
249	17	2.6	397	5	ABV37453	Abv37453 Human pro	c 306	17	2.6	697	4	ABL15733	AbL15733 Drosophi1
250	17	2.6	408	5	ABV09966	Abv09966 Human pro	c 307	17	2.6	707	4	AAH34792	Aah34792 Human col
251	17	2.6	408	5	ABV00924	Abv00924 Human pro	c 308	17	2.6	730	4	AAS28560	Aas28560 Genomic s
252	17	2.6	415	5	ABV00797	Abv00797 Human pro	c 309	17	2.6	747	5	AAH89648	Aah89648 DNA enco
253	17	2.6	416	4	AA192616	AA192616 Human pol	c 310	17	2.6	748	5	AAH93166	Aah93166 DNA enco
254	17	2.6	433	5	ABV31265	Abv31265 Human pro	c 311	17	2.6	767	4	AAK58473	Aak58473 Human imm
255	17	2.6	437	4	ADJ16740	Adj16740 Human nov	312	17	2.6	785	5	ABV26371	Abv26371 Human pro
256	17	2.6	437	4	ABV06618	Abv06618 Human cDN	313	17	2.6	785	5	ABV26451	Abv26451 Human pro
257	17	2.6	437	5	ABA13498	AbA13498 Human ner	314	17	2.6	785	5	ABV20532	Abv20532 Human pro
258	17	2.6	437	6	ABN65612	Abn65612 Human can	315	17	2.6	785	5	ABV20610	Abv20610 Human pro
259	17	2.6	437	6	ABV83955	Abv83955 Human pol	c 316	17	2.6	855	6	ABQ48278	Abq48278 Oligonuc
260	17	2.6	437	7	ACA61650	AcA61650 cDNA enco	317	17	2.6	855	6	ABQ48279	Abq48279 Oligonuc
c 261	17	2.6	443	4	AA117153	AA117153 Human bre	318	17	2.6	855	6	ACB30317	AcB30317 Prokaryot
262	17	2.6	452	5	ABV40234	Abv40234 Human pro	c 319	17	2.6	867	6	ABK78996	Abk78996 Bacillus
263	17	2.6	452	5	ABV31140	Abv31140 Human pro	c 320	17	2.6	872	6	ABQ34616	Abq34616 Oligonuc
264	17	2.6	452	5	ABV40108	Abv40108 Human pro	321	17	2.6	872	6	ABQ34617	Abq34617 Oligonuc
265	17	2.6	456	6	ABSO5460	Abso5460 Human gen	c 322	17	2.6	880	4	AAH99204	Aah99204 Human pro
266	17	2.6	468	2	AAV86346	AAv86346 EST clone	c 323	17	2.6	930	4	ABA09243	AbA09243 Human sec
267	17	2.6	473	6	ABK79421	Abk79421 Bacillus	c 324	17	2.6	930	4	AAK53129	Aak53129 Human sec
c 268	17	2.6	483	6	ABV94025	Abv94025 Breast ca	c 325	17	2.6	1001	3	AAK53129	Aak53129 Human sec
269	17	2.6	498	6	ABN65290	Abn65290 Human can	c 326	17	2.6	1020	6	ABQ27514	Abq27514 Oligonuc
c 270	17	2.6	503	6	ABV57161	Abv57161 Human pro	c 327	17	2.6	1020	6	ABQ27515	Abq27515 Oligonuc
c 271	17	2.6	503	6	ABQ31106	Abq31106 Oligonuc	328	17	2.6	1063	4	ABN06362	Abn06362 Human cDN
c 272	17	2.6	503	6	ABQ31107	Abq31107 Oligonuc	329	17	2.6	1063	6	ABN06369	Abn06369 Human cDN
c 273	17	2.6	513	4	ABA61907	AbA61907 Human fce	330	17	2.6	1083	7	ACB30755	AcB30755 Prokaryot
c 274	17	2.6	513	4	AAK36116	AaK36116 Human bon	331	17	2.6	1089	3	AAK41880	Aak41880 Arabidops
c 275	17	2.6	513	4	AAK10218	AAk10218 Human bra	332	17	2.6	1091	3	AAK50956	Aak50956 Arabidops
c 276	17	2.6	526	6	ABQ92790	Abq92790 Trifletum	c 333	17	2.6	1096	4	AAJ16737	Aaj16737 Human nov
c 277	17	2.6	527	6	ABT07906	Abt07906 Human lun	c 334	17	2.6	1096	7	ACA61647	AcA61647 cDNA enco
c 278	17	2.6	552	6	ABQ16336	Abq16336 Oligonuc	335	17	2.6	1098	6	ABQ46497	Abq46497 Oligonuc
c 279	17	2.6	552	6	ABQ16337	Abq16337 Oligonuc	c 336	17	2.6	1098	6	ABQ46496	Abq46496 Oligonuc
c 280	17	2.6	561	7	ACA27984	AcA27984 Prokaryot	337	17	2.6	1112	6	ABK79021	Abk79021 Bacillus
c 281	17	2.6	579	6	ABV53656	Abv53656 Human pro	338	17	2.6	1182	8	ADA28927	Ada28927 DNA enco
c 282	17	2.6	585	5	ABT07907	Abt07907 Human lun	339	17	2.6	1269	6	ABQ41990	Abq41990 Candida a
c 283	17	2.6	585	5	AA571445	AA571445 DNA enco	340	17	2.6	1269	6	ABQ41991	Abq41991 Oligonuc
c 284	17	2.6	586	5	ABV59028	Abv59028 Human pro	c 341	17	2.6	1272	6	ABN83226	Abn83226 Human hee
c 285	17	2.6	588	6	ABQ40397	Abq40397 Oligonuc	342	17	2.6	1286	3	AAZ61504	Aaz61504 DNA enco
c 286	17	2.6	588	6	ABQ40396	Abq40396 Oligonuc	343	17	2.6	1302	7	ACF74547	Acf74547 Stephyloc
c 287	17	2.6	590	6	ABD35081	Abd35081 Mouse mit	344	17	2.6	1336	6	ABV77611	Abv77611 Serine th
c 288	17	2.6	591	3	AAK79274	AAk79274 Human lun	c 345	17	2.6	1354	6	ABZ11583	Abz11583 Human pol
c 289	17	2.6	591	3	AAK23350	AAk23350 Human lun	c 346	17	2.6	1356	7	ADA67847	Ada67847 Arabidops
c 290	17	2.6	591	9	ADD66624	Add66624 Human lun	c 347	17	2.6	1374	7	ACA30203	AcA30203 Prokaryot
c 291	17	2.6	591	9	ADD66624	Add66624 Human lun	348	17	2.6				
c 292	17	2.6	620	6	ABQ48336	Abq48336 Oligonuc	349	17	2.6				

c 350	17	2.6	1403	7	ADA72445	Ada72445	Rice gene	407	17	2.6	4163	6	ABL34331	Ab134331	Human imm
c 351	17	2.6	1770	3	AAFI35968	Aafi35968	Human pro	408	17	2.6	4190	6	ABL32443	Ab132443	Human imm
c 352	17	2.6	1526	9	ADDO5234	Ado5234	Adenylation	409	17	2.6	4190	9	ADB69149	Abd69149	C. neofor
c 353	17	2.6	1538	3	AAQ47155	Aaq47155	Arabidops	410	17	2.6	4227	4	ABL18518	Ab118518	Arabidops
c 354	17	2.6	1622	9	ADBS7516	Adbs7516	Human gen	411	17	2.6	4231	5	ABV24836	Abv24836	Human pro
c 355	17	2.6	1622	9	ADBS7520	Adbs7520	Human gen	412	17	2.6	4231	5	ABV28175	Abv28175	Human pro
c 356	17	2.6	1795	4	AAH76414	Aah76414	RGS prote	413	17	2.6	4231	5	ABV23325	Abv23325	Human pro
c 357	17	2.6	1857	6	ABQ67921	Abq67921	Listeria	414	17	2.6	4263	4	ABL18878	Ab118878	Human pro
c 358	17	2.6	1857	6	ABQ69940	Abq69940	Listeria	415	17	2.6	4554	7	ACA30282	Acc30282	Prokaryot
c 359	17	2.6	1858	7	ABT42965	Abt42965	Human neu	416	17	2.6	4930	6	ABK92231	Abk92231	Prostate
c 360	17	2.6	1911	6	ABL34257	Ab134257	Human imm	417	17	2.6	5033	4	AA546374	Aas46374	Tumour su
c 361	17	2.6	1938	9	ADCA32181	Adc32181	Human nov	418	17	2.6	5209	6	ABL32186	Ab132186	Human imm
c 362	17	2.6	1949	2	AAK33531	Aak33531	Rice beta	419	17	2.6	5252	6	ABL33135	Ab133135	Human imm
c 363	17	2.6	2000	6	ABE16206	Ab216206	Arabidops	420	17	2.6	5269	6	ABL34056	Ab134056	Human imm
c 364	17	2.6	2000	6	ABE15378	Ab215378	Arabidops	421	17	2.6	5271	2	AAK20505	Aak20505	Polynucle
c 365	17	2.6	2000	6	ABE15499	Ab215499	Arabidops	422	17	2.6	5273	6	ABL32874	Ab132874	Human imm
c 366	17	2.6	2000	6	ABE16827	Ab216827	Arabidops	423	17	2.6	5291	4	ABL07282	Ab107282	Drosophill
c 367	17	2.6	2000	6	ABE15642	Ab215642	Arabidops	424	17	2.6	5304	6	ABK28356	Abk28356	DNA trans
c 368	17	2.6	2000	6	ABE16940	Ab216940	Arabidops	425	17	2.6	5307	6	ABK40043	Abk40043	Human che
c 369	17	2.6	2000	7	ADM73466	Adm73466	Rice gene	426	17	2.6	5307	6	ABL70393	Ab170393	Chemical cell
c 370	17	2.6	2000	7	ADA73412	Ada73412	Rice gene	427	17	2.6	5313	6	ABL32762	Ab132762	Human imm
c 371	17	2.6	2000	7	ADA72746	Ada72746	Rice gene	428	17	2.6	5347	6	ABL33668	Ab133668	Human imm
c 372	17	2.6	2000	7	ADA69320	Ada69320	Rice gene	429	17	2.6	5406	6	ABL33099	Ab133099	Human imm
c 373	17	2.6	2000	7	ADA72067	Ada72067	Rice gene	430	17	2.6	5429	5	AAE28637	Aae28637	Human imm
c 374	17	2.6	2023	5	AA582278	Aa582278	DNA encod	431	17	2.6	5429	5	AAE28637	Aae28637	Human imm
c 375	17	2.6	2135	7	ACM28888	Acc28888	Prokaryot	432	17	2.6	5437	6	AAE28536	Aae28536	Arabidops
c 376	17	2.6	2190	9	ADG90689	Adg90689	E. faeculi	433	17	2.6	5454	3	AAAT0236	Aaa70236	Human imm
c 377	17	2.6	2276	6	ABL60317	Ab160317	Human DNA	434	17	2.6	5460	6	ABL33904	Ab133904	Human imm
c 378	17	2.6	2285	4	ABL22808	Ab122808	Drosophill	435	17	2.6	5477	6	ABK34021	Abk34021	Human DNA
c 379	17	2.6	2306	4	ABL08362	Ab108362	Drosophill	436	17	2.6	5477	7	ADK20445	Adk20445	Prostate
c 380	17	2.6	2339	4	ABL21948	Ab21948	Drosophill	437	17	2.6	5477	7	ADK20445	Adk20445	Prostate
c 381	17	2.6	2369	2	AAI99557	Aai99557	Phytolacc	438	17	2.6	5491	4	AA546390	Aa546390	Tumour su
c 382	17	2.6	2369	2	ABA96543	Ab196543	Phytolacc	439	17	2.6	5659	6	ABL32796	Ab132796	Human imm
c 383	17	2.6	2392	4	ABL15536	Ab115536	Drosophill	440	17	2.6	5683	6	ABL34591	Ab134591	Human met
c 384	17	2.6	2400	6	ABL34366	Aa34366	Human imm	441	17	2.6	5683	6	ABL34591	Ab134591	Human met
c 385	17	2.6	2475	5	AA581626	Aa581626	DNA encod	442	17	2.6	5683	6	ABL70400	Ab170400	Chemical cell
c 386	17	2.6	2493	6	ABE14764	Ab214764	Arabidops	443	17	2.6	5683	9	ADB54310	Abd54310	Pretearte
c 387	17	2.6	2567	4	ABL27850	Ab127850	Drosophill	444	17	2.6	5683	9	ADB54310	Abd54310	Pretearte
c 388	17	2.6	2594	2	AAK13249	Aak13249	Enterococ	445	17	2.6	5693	4	ABQ67148	Abq67148	Human eng
c 389	17	2.6	2594	6	ABE99044	Ab99044	Enterococ	446	17	2.6	5729	6	ABQ67148	Abq67148	Human eng
c 390	17	2.6	2711	4	ABL14890	Ab114890	Drosophill	447	17	2.6	5750	4	AA546709	Aa546709	Tumour su
c 391	17	2.6	2831	2	AAQ03183	Aaq03183	Pyruvate-	448	17	2.6	5750	6	ABL34009	Ab134009	Human imm
c 392	17	2.6	2847	4	ABL22560	Ab122560	Drosophill	449	17	2.6	5763	6	ABL32182	Ab132182	Human imm
c 393	17	2.6	2885	2	AAQ02803	Aaq02803	Pyruvate	450	17	2.6	5769	6	ABK40019	Abk40019	Human imm
c 394	17	2.6	2885	2	AAI96632	Aai96632	DNA encod	451	17	2.6	5770	4	ABL19024	Ab119024	Human che
c 395	17	2.6	2899	9	ADD48969	Ad48969	Rat gene	452	17	2.6	5781	4	AA527714	Aa527714	Drosophill
c 396	17	2.6	2922	9	ADC58115	Adc58115	Caenorhab	453	17	2.6	5781	9	ADB94517	Abd94517	Novel hum
c 397	17	2.6	2982	4	ABL15732	Ab115732	S. opidier	454	17	2.6	5782	4	AA527715	Aa527715	DNA encod
c 398	17	2.6	3065	4	AAH54366	Aah54366	S. opidier	455	17	2.6	5782	4	AA527715	Aa527715	DNA encod
c 399	17	2.6	3366	3	AAH70175	Aah70175	Plasmodiu	456	17	2.6	5879	6	ADB94518	Abd94518	Novel hum
c 400	17	2.6	3692	4	AAH74295	Aah74295	S. cerevis	457	17	2.6	5883	6	ABL32268	Ab132268	Human imm
c 401	17	2.6	3739	3	AAH81547	Aa81547	N. mening	458	17	2.6	5886	6	ABL32733	Ab132733	Human imm
c 402	17	2.6	3742	2	AAV61172	Aav61172	cDNA from	459	17	2.6	5975	6	ABL32237	Ab132237	Human imm
c 403	17	2.6	3840	3	AAAC60046	Aac60046	Human sec	460	17	2.6	5984	6	ABQ66994	Abq66994	Human eng
c 404	17	2.6	3855	7	ACA52780	Acc52780	Prokaryot	461	17	2.6	6046	4	AA545311	Aa545311	Chemical cell
c 405	17	2.6	3948	4	ABLO9642	Ab109642	Drosophill	462	17	2.6	6046	6	ABK28150	Abk28150	DNA trans
c 406	17	2.6	4118	4	ABLO3892	Ab103892	Drosophill	463	17	2.6	6048	4	AA546614	Aa546614	Tumour su

464	17	2.6	6061	4	AA545335	521	17	2.6	6988	6	ABL34441	ABL34441	Human imm
465	17	2.6	6065	6	ABK31357	522	17	2.6	7011	6	ABK39940	ABK39940	Human che
466	17	2.6	6065	6	ABL70580	523	17	2.6	7011	6	ABL32546	ABL32546	Human imm
467	17	2.6	6065	6	AA561261	524	17	2.6	7025	6	ABK40060	ABK40060	Human che
468	17	2.6	6070	6	ABL33678	525	17	2.6	7025	6	AA563351	AA563351	Chemical
469	17	2.6	6070	6	ABL34578	526	17	2.6	7049	6	ABL32157	ABL32157	Human imm
470	17	2.6	6070	6	ABL70371	527	17	2.6	7049	6	ABL54306	ABL54306	Chemical
471	17	2.6	6070	6	ABQ67129	528	17	2.6	7225	4	ABL01994	ABL01994	Human imm
472	17	2.6	6104	6	AA546296	529	17	2.6	7351	6	ABL32028	ABL32028	Human imm
473	17	2.6	6104	6	ABL32297	530	17	2.6	7430	2	AAV31250	AAV31250	E. coli J
474	17	2.6	6104	9	ADB54104	531	17	2.6	7456	6	ABL33930	ABL33930	Human imm
475	17	2.6	6104	9	ADB54232	532	17	2.6	7456	6	ABL92292	ABL92292	Chemical
476	17	2.6	6106	4	AA546429	533	17	2.6	7456	6	ABL33784	ABL33784	Human imm
477	17	2.6	6106	6	ABK40031	534	17	2.6	7511	6	ABL33283	ABL33283	Human imm
478	17	2.6	6107	6	ABL33472	535	17	2.6	7522	6	ABL32914	ABL32914	Human imm
479	17	2.6	6107	6	ABK31431	536	17	2.6	7560	6	ABL33222	ABL33222	Human imm
480	17	2.6	6107	6	ABL70390	537	17	2.6	7631	6	ABL33861	ABL33861	Human imm
481	17	2.6	6107	6	AA561342	538	17	2.6	7659	6	ABL32189	ABL32189	Human imm
482	17	2.6	6115	6	ABL33801	539	17	2.6	7771	6	ABL33973	ABL33973	Human imm
483	17	2.6	6121	6	ABL33974	540	17	2.6	7819	6	ABL33953	ABL33953	Human imm
484	17	2.6	6127	6	ABL33615	541	17	2.6	7819	6	ABL34607	ABL34607	Human met
485	17	2.6	6134	6	ABL33615	542	17	2.6	7906	6	AA545391	AA545391	Chemical
486	17	2.6	6138	4	ABL10128	543	17	2.6	7906	6	ABK28236	ABK28236	DNA trans
487	17	2.6	6143	4	AA107041	544	17	2.6	7906	6	ABK80179	ABK80179	Human che
488	17	2.6	6174	6	ABL33509	545	17	2.6	8129	4	AA546764	AA546764	Tumour su
489	17	2.6	6174	6	ABD28393	546	17	2.6	8168	6	ABL32929	ABL32929	Human imm
490	17	2.6	6216	6	ABK39932	547	17	2.6	8168	6	AA563329	AA563329	Chemical
491	17	2.6	6216	6	ABL70139	548	17	2.6	8201	6	ABL32307	ABL32307	Human imm
492	17	2.6	6222	6	ABL32238	549	17	2.6	8201	6	ABL54328	ABL54328	Chemical
493	17	2.6	6227	6	ABL34499	550	17	2.6	8237	4	AA546802	AA546802	Tumour su
494	17	2.6	6227	6	ABL70176	551	17	2.6	8323	4	ABL32058	ABL32058	Human imm
495	17	2.6	6228	6	ABK31966	552	17	2.6	8346	6	ABK28328	ABK28328	DNA trans
496	17	2.6	6228	6	ABL70469	553	17	2.6	8372	4	AA546353	AA546353	Tumour su
497	17	2.6	6228	6	AA561430	554	17	2.6	8467	6	ABL32109	ABL32109	Human imm
498	17	2.6	6277	4	AA546729	555	17	2.6	8530	6	ABL33755	ABL33755	Human imm
499	17	2.6	6277	4	ABL34041	556	17	2.6	8530	6	ABK31415	ABK31415	Signal tr
500	17	2.6	6286	4	AA546592	557	17	2.6	8551	5	AA572863	AA572863	DNA encod
501	17	2.6	6306	4	AA545515	558	17	2.6	8592	6	ABL33982	ABL33982	Human imm
502	17	2.6	6306	6	ABK28457	559	17	2.6	8614	4	AAK74343	AAK74343	Human imm
503	17	2.6	6368	6	ABL33939	560	17	2.6	8771	6	ABL33824	ABL33824	Human imm
504	17	2.6	6368	6	ABL92299	561	17	2.6	8805	6	ABL32513	ABL32513	Human imm
505	17	2.6	6368	6	ABL49368	562	17	2.6	9018	6	ABK31256	ABK31256	Signal tr
506	17	2.6	6408	4	AAK89966	563	17	2.6	9018	6	ABL70211	ABL70211	Chemical
507	17	2.6	6413	4	AA546362	564	17	2.6	9018	6	AA561166	AA561166	Human che
508	17	2.6	6413	6	ABQ67000	565	17	2.6	9018	6	ABK80078	ABK80078	Human che
509	17	2.6	6464	6	ABL32514	566	17	2.6	9180	6	ABL33964	ABL33964	Human imm
510	17	2.6	6509	6	ABL32227	567	17	2.6	9206	6	ABL33674	ABL33674	Human imm
511	17	2.6	6561	6	ABN80021	568	17	2.6	9238	6	ABK28365	ABK28365	DNA trans
512	17	2.6	6564	6	ABL32123	569	17	2.6	9306	4	ABL12980	ABL12980	Drosophila
513	17	2.6	6566	6	ABK28350	570	17	2.6	9493	2	AAAT59129	AAAT59129	Hepatitis
514	17	2.6	6590	6	ABL33477	571	17	2.6	9493	3	AA55375	AA55375	Hepatitis
515	17	2.6	6668	4	AA546418	572	17	2.6	9547	6	ABL33504	ABL33504	Human imm
516	17	2.6	6668	6	ABN33219	573	17	2.6	9707	6	ABL33421	ABL33421	Human imm
517	17	2.6	6668	6	ABN80163	574	17	2.6	9760	6	ABK31242	ABK31242	Signal tr
518	17	2.6	6692	4	AA546610	575	17	2.6	9760	6	ABL70197	ABL70197	Chemical
519	17	2.6	6907	6	ABL32366	576	17	2.6	9760	6	ABL70197	ABL70197	Chemical
520	17	2.6	6977	4	AA546628	577	17	2.6	9760	6	AA561155	AA561155	Human gen

578	17	2.6	9859	6	ABL34132	Ab134132 Human Imm	c 635	17	2.6	16602	6	ABN80068	Abn80068 Human che
c 579	17	2.6	9869	4	AAE59947	AAe59947 Human TNF	c 636	17	2.6	16633	6	ABN79984	Abn79984 Human che
c 580	17	2.6	9898	2	AAV20767	AAv20767 Human OCI	c 637	17	2.6	16720	6	ABL32415	Ab132415 Human Imm
c 581	17	2.6	9997	6	ABL32369	Ab132369 Human Imm	c 638	17	2.6	16720	6	AA561119	AAe61119 Human gen
c 582	17	2.6	9997	6	ABL34485	Ab134485 Human met	c 639	17	2.6	16766	6	ABL34156	Ab134156 Human Imm
c 583	17	2.6	10190	2	AA733183	AA733183 Fragment	c 640	17	2.6	17280	4	AA546772	AAe46772 Human Imm
c 584	17	2.6	10231	8	ACR03989	ACr03989 Human cDN	c 641	17	2.6	17419	4	AA545393	AAe45393 Human Imm
585	17	2.6	10329	6	ABL34123	Ab134123 Human Imm	c 642	17	2.6	17419	6	ABL33295	Ab133295 Human Imm
586	17	2.6	10609	4	AA546560	AAe46560 Tumour su	c 643	17	2.6	17419	6	ABK28238	Abk28238 Human Imm
587	17	2.6	10609	6	ABK31269	Abk31269 Signal tr	c 644	17	2.6	17594	6	ABL34027	Ab134027 Human Imm
c 589	17	2.6	10710	6	ABL32892	Ab132892 Human Imm	c 645	17	2.6	18218	6	ABL33949	Ab133949 Human Imm
c 590	17	2.6	10716	6	ABL33419	Ab133419 Human Imm	c 646	17	2.6	18318	6	ABL33948	Ab133948 Human Imm
591	17	2.6	10996	6	AA546806	AAe46806 Tumour su	c 647	17	2.6	18357	6	AB067083	ABe67083 Human Imm
592	17	2.6	10996	6	ABK28466	ABk28466 DNA trans	c 648	17	2.6	18359	2	AAK20255	AAk20255 Borrelia
593	17	2.6	11691	6	ABL34241	Ab134241 Human Imm	c 649	17	2.6	18512	6	ABL32977	Ab132977 Human Imm
c 594	17	2.6	12054	6	ABL33178	Ab133178 Human Imm	c 650	17	2.6	18683	6	ABL32312	Ab132312 Human Imm
c 595	17	2.6	12069	6	ABK39930	ABk39930 Human che	c 651	17	2.6	18683	6	ABL54333	ABL54333 Chemocell
c 596	17	2.6	12177	6	ABL32650	Ab132650 Human Imm	c 652	17	2.6	18988	4	AA546342	AAe46342 Tumour su
597	17	2.6	12356	4	AA546509	AAe46509 Tumour su	c 653	17	2.6	18988	6	ABL32701	Ab132701 Human Imm
598	17	2.6	12865	2	AAV62292	AAv62292 Human Int	c 654	17	2.6	18988	6	ABL34509	Ab134509 Human met
599	17	2.6	12865	2	AAV75925	AAv75925 Human Int	c 655	17	2.6	18988	6	ABL70204	Ab170204 Chemocell
600	17	2.6	12865	2	ABX15530	ABx15530 Human Int	c 656	17	2.6	19082	6	ABL32627	Ab132627 Human Imm
601	17	2.6	12865	3	AAE63769	AAe63769 Human IL-	c 657	17	2.6	19087	6	ABL32793	Ab132793 Human Imm
602	17	2.6	12865	4	AAE27667	AAe27667 IL-1RN DN	c 658	17	2.6	19233	6	ABL48345	ABL48345 Human pol
603	17	2.6	12865	5	AAE91435	AAe91435 Human IL-	c 659	17	2.6	19429	4	AA530443	AAe30443 DNA encod
604	17	2.6	12865	7	ADJ51465	ADd51465 Human Int	c 660	17	2.6	19429	4	AAK71692	AAk71692 Human Imm
605	17	2.6	12865	7	ACC44353	ACc44353 Human Int	c 661	17	2.6	19429	4	AAI06223	AAI06223 Human rep
606	17	2.6	12865	7	AAJ54517	AAj54517 Secreted	c 662	17	2.6	19429	5	ABAI4454	ABa14454 Human rep
607	17	2.6	13131	6	ABL52249	Ab152249 Chemocell	c 663	17	2.6	19459	6	ABK31212	ABk31212 Signal tr
c 608	17	2.6	13131	6	ABL05342	Ab105342 Drosophill	c 664	17	2.6	19459	6	ABH70527	ABh70527 Chemocell
c 609	17	2.6	13453	6	ABN80176	ABn80176 Human che	c 665	17	2.6	19653	6	ABL33335	Ab133335 Human Imm
610	17	2.6	13511	6	ABL32280	Ab132280 Human Imm	c 666	17	2.6	20300	4	AA530441	AAe30441 DNA encod
611	17	2.6	13574	6	ABL33316	Ab133316 Human Imm	c 667	17	2.6	20300	4	AAK71686	AAk71686 Human Imm
612	17	2.6	13584	6	ABL32615	Ab132615 Human Imm	c 668	17	2.6	20300	5	AAI06221	AAI06221 Human rep
c 613	17	2.6	13584	6	ABL32614	Ab132614 Human Imm	c 669	17	2.6	20300	5	ABAI4452	ABa14452 Human rep
614	17	2.6	13724	4	AB114676	Ab114676 Drosophill	c 670	17	2.6	20566	4	AAK75098	AAk75098 Human Imm
615	17	2.6	13792	6	ABL33571	Ab133571 Human Imm	c 671	17	2.6	20752	4	AAK75098	AAk75098 Human Imm
616	17	2.6	14147	4	AA546744	AAe46744 Tumour su	c 672	17	2.6	21537	6	ABL33999	Ab133999 Human Imm
617	17	2.6	14147	6	ABK33956	ABk33956 Human DNA	c 673	17	2.6	21667	4	AA530368	AAe30368 Human Imm
618	17	2.6	14147	7	ADA20387	ADa20387 Prostate	c 674	17	2.6	22008	4	AA536610	AAe36610 Human Imm
619	17	2.6	14147	7	ADA84194	ADa84194 Human ren	c 675	17	2.6	22008	5	ABAI5839	ABa15839 Human car
620	17	2.6	14147	9	ADB54098	ADb54098 Pretrearte	c 676	17	2.6	22008	7	ABT16888	ABt16888 Human sec
621	17	2.6	14147	9	ADB54226	ADb54226 Pretrearte	c 677	17	2.6	22008	7	ABE67377	ABe67377 Human sec
622	17	2.6	14147	9	ADB84164	ADb84164 Human lym	c 678	17	2.6	22008	7	ABE73783	ABe73783 Secreted
623	17	2.6	14147	9	ADB84088	ADb84088 Human lym	c 679	17	2.6	22008	7	ADN98459	ADn98459 Human sec
624	17	2.6	14712	6	ABN80249	ABn80249 Human che	c 680	17	2.6	22008	9	ADC20627	ADc20627 Human sec
625	17	2.6	15435	4	AB114186	Ab114186 Drosophill	c 681	17	2.6	22008	9	ADC47304	ADc47304 Human car
626	17	2.6	15435	6	ABL34154	Ab134154 Human Imm	c 682	17	2.6	22140	4	AA530444	AAe30444 DNA encod
627	17	2.6	15698	6	ABL34141	Ab134141 Human Imm	c 683	17	2.6	22140	4	AAK71693	AAk71693 Human Imm
628	17	2.6	15743	6	ABK28395	ABk28395 DNA trans	c 684	17	2.6	22140	4	AAI06624	AAI06624 Human rep
c 629	17	2.6	15853	6	AB170466	ABi70466 Chemocell	c 685	17	2.6	22140	5	ABAI4455	ABa14455 Human rep
c 630	17	2.6	15853	6	AA561457	AAe61457 Human gen	c 686	17	2.6	22141	4	AA530442	AAe30442 DNA encod
631	17	2.6	15861	6	ABL32524	Ab132524 Human Imm	c 687	17	2.6	22141	4	AAK71689	AAk71689 Human Imm
632	17	2.6	16579	9	ADB54246	ADb54246 Pretrearte	c 688	17	2.6	22141	5	ABAI4453	ABa14453 Human rep
633	17	2.6	16579	9	ADB54246	ADb54246 Pretrearte	c 689	17	2.6	22141	5	ABAI4453	ABa14453 Human rep
c 634	17	2.6	16602	6	ABL32726	Ab132726 Human Imm	c 690	17	2.6	23210	4	AAE28530	AAe28530 Genomic f
							c 691	17	2.6	23683	6	ABL34622	Ab134622 Human met

692	17	2.6	23683	6	ABL70481	Ab170481	Chemical1	749	17	2.6	94529	8	ADA03086	Ada03086	Human hCG
693	17	2.6	23695	6	ABG66882	AbG66882	Human ang	750	17	2.6	94529	9	ADB72824	ADB72824	Human hCG
694	17	2.6	23695	6	ABG66882	AbG66882	Human ang	750	17	2.6	94529	9	ADB72824	ADB72824	Human hCG
695	17	2.6	24639	6	ABL70569	Ab170569	Chemical1	751	17	2.6	94531	8	ADA66370	Ada66370	Human hCG
696	17	2.6	25655	4	AAK76405	AAK76405	Human imm	752	17	2.6	95769	7	ADA66659	Ada66659	Arbaldops
697	17	2.6	26197	4	ABK43078	ABK43078	Genomic s	753	17	2.6	96595	8	ADA02936	Ada02936	Human BRA
698	17	2.6	26197	8	ADB61234	ADB61234	Connectiv	754	17	2.6	96595	9	ADB72674	ADB72674	Human BRA
699	17	2.6	26210	4	ABK43079	ABK43079	Genomic s	755	17	2.6	96595	9	ADB72674	ADB72674	Human BRA
700	17	2.6	26210	4	ADB61235	ADB61235	Connectiv	756	17	2.6	96596	8	ADA02834	Ada02834	Human BRA
701	17	2.6	27156	8	ADA02870	ADA02870	Human gat	757	17	2.6	96596	9	ADB72572	ADB72572	Human BRA
702	17	2.6	27156	9	ADA02870	ADA02870	Human gat	758	17	2.6	96596	9	ADB72572	ADB72572	Human BRA
703	17	2.6	28413	9	ADC51646	ADC51646	BmNPV gen	759	17	2.6	96597	9	ADC85340	Adc85340	Human Lmo
704	17	2.6	28564	9	ADA8574	ADA8574	Human gen	760	17	2.6	96597	9	ADC85340	Adc85340	Human Lmo
705	17	2.6	28564	9	ADA8574	ADA8574	Human gen	761	17	2.6	96597	9	ADC85340	Adc85340	Human Lmo
706	17	2.6	28720	4	ABL07302	ABL07302	Human nov	762	17	2.6	96598	8	ADA02861	Ada02861	Mouse Itp
707	17	2.6	28993	9	ADB37662	ADB37662	Human che	763	17	2.6	96598	9	ADB72599	ADB72599	Mouse Itp
708	17	2.6	29993	9	ADB37660	ADB37660	Human che	764	17	2.6	96598	9	ADB72599	ADB72599	Mouse Itp
709	17	2.6	32038	4	AAK90877	AAK90877	Human dig	765	17	2.6	97658	7	ABG8210_3	ABG8210_3	Continuation (4 of
710	17	2.6	32038	4	AAK99880	AAK99880	Human dig	766	17	2.6	97658	7	ABG8210_3	ABG8210_3	Continuation (4 of
711	17	2.6	32038	4	AAK99880	AAK99880	Human dig	767	17	2.6	110000	2	AAZ01425_07	AAZ01425_07	Continuation (8 of
712	17	2.6	32038	5	AAK99880	AAK99880	Human dig	768	17	2.6	110000	2	AAK91990_03	AAK91990_03	Continuation (4 of
713	17	2.6	32154	4	AAK33028	AAK33028	Human nov	769	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
714	17	2.6	32154	4	AAK33028	AAK33028	Human nov	770	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
715	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
716	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
717	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
718	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
719	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
720	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
721	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
722	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
723	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
724	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
725	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
726	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
727	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
728	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
729	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
730	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
731	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
732	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
733	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
734	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
735	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
736	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
737	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
738	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
739	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
740	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
741	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
742	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
743	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
744	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
745	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
746	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
747	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of
748	17	2.6	32154	4	AAK33028	AAK33028	Human nov	771	17	2.6	110000	6	AAK81490_01	AAK81490_01	Continuation (2 of

806	16	2.5	42	2	AA035784	AA035784 H6 Promot	c 863	16	2.5	307	5	ABV61121	ABV61121 Human pro
c 807	16	2.5	46	6	AB565299	AB565299 A. thelia	864	16	2.5	311	7	ADA83947	ADA83947 Human POM
808	16	2.5	53	6	ABK53142	ABK53142 HIV-1 rev	865	16	2.5	316	4	AA089750	AA089750 Human gas
c 809	16	2.5	53	6	AA145504	AA145504 HIV-1 pol	c 866	16	2.5	319	4	AA538003	AA538003 Novel hum
c 810	16	2.5	83	6	ABK45880	ABK45880 cDNA enco	c 867	16	2.5	324	5	ABV43377	ABV43377 Human pro
c 811	16	2.5	97	3	AA011023	AA011023 Human sec	c 868	16	2.5	326	5	ABV15088	ABV15088 Human pro
c 812	16	2.5	99	3	AA015302	AA015302 Human sec	c 869	16	2.5	326	5	ABV15089	ABV15089 Human ner
c 813	16	2.5	108	3	AA012250	AA012250 Human sec	c 870	16	2.5	330	5	AA050736	AA050736 Cervical
c 814	16	2.5	137	2	AA086489	AA086489 Human sin	c 871	16	2.5	332	5	AA050736	AA050736 Cervical
c 815	16	2.5	144	2	AA066918	AA066918 Canine he	c 872	16	2.5	342	3	AA024206	AA024206 S. aureus
c 816	16	2.5	144	2	AA066918	AA066918 Canine he	c 873	16	2.5	343	6	ABV94131	ABV94131 Breast ca
c 817	16	2.5	144	2	AA059380	AA059380 Canine he	c 874	16	2.5	344	8	ACH31878	ACH31878 Human end
c 818	16	2.5	146	2	AA075606	AA075606 Canine he	c 875	16	2.5	345	2	AA024640	AA024640 H. pylori
c 819	16	2.5	146	2	AA066916	AA066916 Canine he	c 876	16	2.5	345	2	AA024640	AA024640 H. pylori
c 820	16	2.5	146	2	AA066917	AA066917 Canine he	c 877	16	2.5	345	8	ACH31219	ACH31219 Human bon
c 821	16	2.5	146	2	AA066917	AA066917 Canine he	c 878	16	2.5	345	9	AD061446	AD061446 Rat gene
c 822	16	2.5	146	2	AA066917	AA066917 Canine he	c 879	16	2.5	345	9	AD061446	AD061446 Rat gene
c 823	16	2.5	178	8	ACH16857	ACH16857 Human edu	c 880	16	2.5	345	9	AD061446	AD061446 Rat gene
c 824	16	2.5	189	7	AC074816	AC074816 Staphyloc	c 881	16	2.5	345	9	AD061447	AD061447 Rat gene
c 825	16	2.5	196	4	AA056486	AA056486 Human cDN	c 882	16	2.5	345	9	AD061447	AD061447 Rat gene
c 826	16	2.5	198	2	AA087225	AA087225 EST clone	c 883	16	2.5	347	5	ABV16968	ABV16968 Human ner
c 827	16	2.5	225	2	AA099646	AA099646 Nucleic a	c 884	16	2.5	348	5	ABV12142	ABV12142 Human ner
c 828	16	2.5	225	7	ACA52695	ACA52695 Prokaryot	c 885	16	2.5	348	7	ACA30532	ACA30532 Prokaryot
c 829	16	2.5	226	6	AB008439	AB008439 Human leu	c 886	16	2.5	349	3	AA018144	AA018144 Human sec
c 830	16	2.5	232	4	AA123177	AA123177 Human bre	c 887	16	2.5	350	3	AA002828	AA002828 Human sec
c 831	16	2.5	239	4	ABV74090	ABV74090 Human toe	c 888	16	2.5	351	4	AA011840	AA011840 Human cDN
c 832	16	2.5	239	4	AA154543	AA154543 Probe #23	c 889	16	2.5	352	2	AA088403	AA088403 EST clone
c 833	16	2.5	239	4	AA048713	AA048713 Human bon	c 890	16	2.5	352	5	ABV03304	ABV03304 Human pro
c 834	16	2.5	239	4	AA025466	AA025466 Human bra	c 891	16	2.5	353	5	ABV12473	ABV12473 Human pro
c 835	16	2.5	239	4	ABV48391	ABV48391 Human liv	c 892	16	2.5	356	2	AA007448	AA007448 Rat gene
c 836	16	2.5	239	6	AB022435	AB022435 Human gen	c 893	16	2.5	358	7	ABV53943	ABV53943 Human ES
c 837	16	2.5	251	4	AA016687	AA016687 Human bre	c 894	16	2.5	360	5	ABV00174	ABV00174 Human pro
c 838	16	2.5	252	6	ABV93037	ABV93037 Staphyloc	c 895	16	2.5	371	5	ABV13522	ABV13522 Human pro
c 839	16	2.5	256	4	AA122774	AA122774 Human bre	c 896	16	2.5	372	7	AC073925	AC073925 Staphyloc
c 840	16	2.5	256	4	AA125530	AA125530 Human bre	c 897	16	2.5	372	8	ACH42656	ACH42656 Human foe
c 841	16	2.5	257	3	AA031313	AA031313 Human sec	c 898	16	2.5	380	5	AA094324	AA094324 Human foe
c 842	16	2.5	257	3	AA029304	AA029304 Human sec	c 899	16	2.5	381	5	ABV48090	ABV48090 Human pro
c 843	16	2.5	267	3	AA029557	AA029557 Human sec	c 900	16	2.5	381	7	ACC60361	ACC60361 Rat gene
c 844	16	2.5	276	4	AA087701	AA087701 Human dig	c 901	16	2.5	381	7	ABV55971	ABV55971 Rat gene
c 845	16	2.5	276	6	ABV90040	ABV90040 Human liv	c 902	16	2.5	392	2	AA022296	AA022296 Human mit
c 846	16	2.5	279	7	AC070609	AC070609 Phototrab	c 903	16	2.5	393	2	AA020281	AA020281 Staphyloc
c 847	16	2.5	285	6	AB069802	AB069802 Listeria	c 904	16	2.5	393	2	AA020281	AA020281 Staphyloc
c 848	16	2.5	285	6	AB069802	AB069802 Listeria	c 905	16	2.5	393	3	AA022404	AA022404 Rat gene
c 849	16	2.5	291	4	AA007784	AA007784 Human bre	c 906	16	2.5	393	6	ABV98091	ABV98091 E. faecali
c 850	16	2.5	291	4	AA007784	AA007784 Human bre	c 907	16	2.5	393	7	ABV98091	ABV98091 E. faecali
c 851	16	2.5	295	2	AA083344	AA083344 Breast ca	c 908	16	2.5	393	7	ABV98091	ABV98091 E. faecali
c 852	16	2.5	295	2	AA068885	AA068885 DNA molec	c 909	16	2.5	394	6	ABV94955	ABV94955 Gene #145
c 853	16	2.5	295	6	AA080867	AA080867 Human bre	c 910	16	2.5	396	5	ABV13613	ABV13613 Human pro
c 854	16	2.5	295	6	AA080867	AA080867 Human bre	c 911	16	2.5	396	5	ABV13613	ABV13613 Human pro
c 855	16	2.5	295	6	AA080867	AA080867 Human bre	c 912	16	2.5	396	5	ABV13613	ABV13613 Human pro
c 856	16	2.5	295	6	ABV46757	ABV46757 Human bre	c 913	16	2.5	401	6	ABV64491	ABV64491 Human can
c 857	16	2.5	295	9	AD015207	AD015207 Human bre	c 914	16	2.5	401	6	ABV64491	ABV64491 Human can
c 858	16	2.5	297	3	AA067904	AA067904 Human sec	c 915	16	2.5	406	5	ABV59997	ABV59997 Human pro
c 859	16	2.5	307	2	AA067904	AA067904 Cotton fi	c 916	16	2.5	406	5	ABV59997	ABV59997 Human pro
c 860	16	2.5	307	2	AA067904	AA067904 Cotton fi	c 917	16	2.5	408	4	AA042132	AA042132 Genomic s
c 861	16	2.5	307	2	AA067904	AA067904 Cotton fi	c 918	16	2.5	408	4	AA042132	AA042132 Genomic s
c 862	16	2.5	307	2	AA067904	AA067904 Cotton fi	c 919	16	2.5	408	5	ABV34637	ABV34637 Human pro

920	16	2.5	409	5	ABV15552	Abv15552 Human pro
c 921	16	2.5	411	4	AAK7062	AAK7062 Human 1mm
c 922	16	2.5	411	4	AAK7063	AAK7063 Human 1mm
c 923	16	2.5	411	4	AAI18127	AAI18127 Human pol
c 924	16	2.5	413	7	ACA14166	ACA14166 Prokaryot
c 925	16	2.5	415	4	AB118027	AB118027 Drosophila
c 926	16	2.5	415	5	AAH87801	AAH87801 Peperom
c 927	16	2.5	415	8	ACH49586	ACH49586 Human 1eu
c 928	16	2.5	417	3	AAH30913	AAH30913 Human col
c 929	16	2.5	417	6	ABN91954	ABN91954 StephyLoc
c 930	16	2.5	419	8	ACH49434	ACH49434 Human 1eu
c 931	16	2.5	421	7	ABK52890	ABK52890 Bovine ES
c 932	16	2.5	422	2	AAQ39892	AAQ39892 Expressed
c 933	16	2.5	422	2	AAQ39304	AAQ39304 Human bra
c 934	16	2.5	428	5	ABV04353	ABV04353 Human 1mm
c 935	16	2.5	429	4	AAK74755	AAK74755 Human 1mm
c 936	16	2.5	429	7	ACA21871	ACA21871 Prokaryot
c 937	16	2.5	430	6	ABV83644	ABV83644 Human bre
c 938	16	2.5	434	5	ABA11337	ABA11337 Human ner
c 939	16	2.5	435	3	AAK88403	AAK88403 Rice geno
c 940	16	2.5	435	3	AAK87198	AAK87198 Rice EPS
c 941	16	2.5	435	3	AAK89327	AAK89327 Rice geno
c 942	16	2.5	437	5	ABA16674	ABA16674 Human ner
c 943	16	2.5	438	5	ABA13795	ABA13795 Human ner
c 944	16	2.5	444	7	ABX07983	ABX07983 S. pneumo
c 945	16	2.5	444	7	ACF73774	ACF73774 StephyLoc
c 946	16	2.5	446	4	AAK32585	AAK32585 Human bon
c 947	16	2.5	446	4	AAI187510	AAI187510 Human pol
c 948	16	2.5	446	4	AAK06864	AAK06864 Human bra
c 949	16	2.5	446	4	ABK32296	ABK32296 Human 1lv
c 950	16	2.5	446	6	ABK07374	ABK07374 Human gen
c 951	16	2.5	447	7	ABK45796	ABK45796 Bovine ES
c 952	16	2.5	448	4	AAI186534	AAI186534 Human pol
c 953	16	2.5	448	5	ABV57496	ABV57496 Human pro
c 954	16	2.5	449	6	ABK91769	ABK91769 DNA encod
c 955	16	2.5	449	8	ACH15987	ACH15987 Human fce
c 956	16	2.5	452	4	ABA56642	ABA56642 Human fce
c 957	16	2.5	452	4	ABA46094	ABA46094 Human bre
c 958	16	2.5	452	4	ABA26249	ABA26249 Probe #47
c 959	16	2.5	452	4	AAK30302	AAK30302 Human bon
c 960	16	2.5	452	4	AAK04780	AAK04780 Human fce
c 961	16	2.5	453	5	AAI04684	AAI04684 Probe #46
c 962	16	2.5	453	5	AAH88048	AAH88048 Peperom
c 963	16	2.5	453	6	ABV76271	ABV76271 Human ORF
c 964	16	2.5	456	8	ACH25736	ACH25736 Human exc
c 965	16	2.5	459	4	AAI199190	AAI199190 Human kid
c 966	16	2.5	459	5	AAI63540	AAI63540 Human fce
c 967	16	2.5	462	8	ACH17965	ACH17965 Human adu
c 968	16	2.5	466	8	ACH26191	ACH26191 Human adu
c 969	16	2.5	467	3	AAH81560	AAH81560 N. mening
c 970	16	2.5	472	8	ACH41782	ACH41782 Human fce
c 971	16	2.5	473	8	ACH25589	ACH25589 Human fce
c 972	16	2.5	478	8	ACH45179	ACH45179 Human fce
c 973	16	2.5	480	8	ACH25709	ACH25709 Human adu
c 974	16	2.5	486	8	ACH25069	ACH25069 Human adu
c 975	16	2.5	486	9	ADD20336	ADD20336 Oreochrom
c 976	16	2.5	486	9	ADD20342	ADD20342 Oreochrom

c 977	16	2.5	487	9	ADE81991	Ade81991 Arabidops
c 978	16	2.5	489	4	AAE17635	AAE17635 Human bre
c 979	16	2.5	489	4	AAE47065	AAE47065 Human bre
c 980	16	2.5	489	6	ABK95100	ABK95100 Human bre
c 981	16	2.5	489	6	ABT08720	ABT08720 Human bre
c 982	16	2.5	489	6	ABK56366	ABK56366 Human bre
c 983	16	2.5	489	7	ABT32878	ABT32878 Human tum
c 984	16	2.5	489	10	ADE44072	Ade44072 Human cDN
c 985	16	2.5	494	4	AAK55617	AAK55617 Human 1mm
c 986	16	2.5	495	5	ABV39043	ABV39043 Human pro
c 987	16	2.5	495	5	ABV44871	ABV44871 Human pro
c 988	16	2.5	496	4	AAK88974	AAK88974 Human dig
c 989	16	2.5	496	5	AAK31843	AAK31843 Human 1lv
c 990	16	2.5	496	6	ABN90198	ABN90198 Human 1lv
c 991	16	2.5	501	9	ACF73041	ACF73041 StephyLoc
c 992	16	2.5	501	9	ADE81627	Ade81627 Arabidops
c 993	16	2.5	503	6	ABK51767	ABK51767 Oligonuc
c 994	16	2.5	503	6	ABK51766	ABK51766 Oligonuc
c 995	16	2.5	507	6	ABK27076	ABK27076 Oligonuc
c 996	16	2.5	507	6	ABK27077	ABK27077 Oligonuc
c 997	16	2.5	507	6	ABK46036	ABK46036 Oligonuc
c 998	16	2.5	507	6	ABK46037	ABK46037 Oligonuc
c 999	16	2.5	507	6	ABK78447	ABK78447 Bacillus
1000	16	2.5	507	7	ABT40677	ABT40677 Toxicity

ALIGNMENTS

RESULT 1						
ID	AAA68249	standard;	DNA;	651	BP.	
AC	AAA68249;					
XX						
DT	15-SEP-2003	(revised)				
DT	05-AUG-2003	(revised)				
DT	27-OCT-2000	(first entry)				
XX						
DE	Bacteriophage 77 77ORF019 nucleotide sequence.					
XX	Bacteriophage; antimicrobial; genome; identification; antibacterial;					
KW	bacterial growth inhibition; bacterial infection; ds.					
OS	Staphylococcus aureus; bacteriophage 77.					
PN	WO200032825-A2.					
XX						
PD	08-JUN-2000.					
XX						
PF	03-DEC-1999;	99WO-1B002040.				
XX						
PR	03-DEC-1998;	98US-0110992P.				
PR	03-JUN-1999;	99US-00326144.				
PR	28-SEP-1999;	99US-00407804.				
PR	30-SEP-1999;	99US-0157218P.				
PR	01-DEC-1999;	99US-0168777P.				

PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX
XX PI Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2000-412361/35.
DR P-PSDB; AAB16524.
XX
XX
XX identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX
XX Disclosure: Page 155; 456pp; English.
XX
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
CC (Updated on 15-SEP-2003 to standardise 05 field)
XX
XX
XX Sequence 651 BP; 275 A; 57 C; 95 G; 224 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 651; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 9.2e-271;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAACGACGAAATATATAGAGCATATATACCTTACGAGAGGTGTCTTTATCA 60
DB 1 ATGAACGACGAAATATATAGAGCATATATACCTTACGAGAGGTGTCTTTATCA 60
QY 61 GTTAAAGATTTTATGATTTTACGATTTTACGATTTTACGATTTTACGATTTT 120
DB 61 GTTAAAGATTTTATGATTTTACGATTTTACGATTTTACGATTTTACGATTTT 120
QY 121 GACCAATATATCGATATATTTAGATTGTTTAAAGGCTAAAGATGATTGGAGCT 180
DB 121 GACCAATATATCGATATATTTAGATTGTTTAAAGGCTAAAGATGATTGGAGCT 180
QY 181 TATATATTCGACGAGACGATGATTTTATGATTTTATGATTTTATGATTTTAT 240
DB 181 TATATATTCGACGAGACGATGATTTTATGATTTTATGATTTTATGATTTTAT 240
QY 241 AATTAGATGAGCAATGTAAGGCTATGAAATGTTATGATTTATGACCAATGATT 300
DB 241 AATTAGATGAGCAATGTAAGGCTATGAAATGTTATGATTTATGACCAATGATT 300
QY 301 AATTATCAATAGATTAAGGCAATGAAATTTTATGATTTATGACCAATGATT 360
DB 301 AATTATCAATAGATTAAGGCAATGAAATTTTATGATTTATGACCAATGATT 360

QY 361 AGTACCAATCAGATTTTATATCTTCTTTGTAAGAAACATGCTATTATAT 420
DB 361 AGTACCAATCAGATTTTATATCTTCTTTGTAAGAAACATGCTATTATAT 420
QY 421 GAAATCAAAAAGATATCTTATTTAAATATATATATATATGATGAAATGA 480
DB 421 GAAATCAAAAAGATATCTTATTTAAATATATATATATATGAAATGA 480
QY 481 GCTTATATCATATGATTTATGATTTATGATTTATGATTTATGATTTAT 540
DB 481 GCTTATATCATATGATTTATGATTTATGATTTATGATTTATGATTTAT 540
QY 541 AATCTTATCTGATTAATTTGAAGACGTTAGTCAAAAAGTTAAATTAACGAACT 600
DB 541 AATCTTATCTGATTAATTTGAAGACGTTAGTCAAAAAGTTAAATTAACGAACT 600
QY 601 TCGATTAAGAAAGATATTTATTTATTTAAACAGAGGATTTAATGA 651
DB 601 TCGATTAAGAAAGATATTTATTTATTTAAACAGAGGATTTAATGA 651
RESULT 2
ID AAB68247 standard; DNA; 41708 BP.
AC AAB68247;
XX
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX Bacteriophage 77 complete genome sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
OS Staphylococcus aureus; bacteriophage 77.
XX
XX WO200032825-A2.
XX
XX 08-JUN-2000.
PD
XX
XX 03-DEC-1999; 99WO-1B002040.
PF
XX
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX PI Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2000-412361/35.
XX

PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Example 3; Page 141-151; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound is active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA68243 to AA69442 and AB16523 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 651; DB 3; Length 41708;

Best Local Similarity 100.0%; Pred. No. 6.9e-211;

Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGACCAATTAATAGGACATATATACCTTAGCAGAGCTGTGCTTTATCA 60
DB 39851 ATGACGACCAATTAATAGGACATATATACCTTAGCAGAGCTGTGCTTTATCA 39910
QY 61 GTTAAAGATTTTACGTAATTTTACAGATCTTACAGATCAAGTAAATCAATTA 120
DB 39911 GTTAAAGATTTTACGTAATTTTACAGATCTTACAGATCAAGTAAATCAATTA 39970
QY 121 GACCAATATATCCGATATATTTAGATTGTTTAAAGGCTAAAGATGTTGAGCT 180
DB 39971 GACCAATATATCCGATATATTTAGATTGTTTAAAGGCTAAAGATGTTGAGCT 40030
QY 181 TATATTATCCAGACGACGATGTAATTTTATGATTTTGAAGTCTTAAAT 240
DB 40031 TATATTATCCAGACGACGATGTAATTTTATGATTTTGAAGTCTTAAAT 40090
QY 241 AATTAGATAGCAAGTAAAGGCTATGAAATGTTATGATTTAGCAATGAT 300
DB 40091 AATTAGATAGCAAGTAAAGGCTATGAAATGTTATGATTTAGCAATGAT 40150
QY 301 AATTATCAAAATAGGTAAGCAATGAAAGTTTAAAGTGAGTTCAACATGATTT 360
DB 40151 AATTATCAAAATAGGTAAGCAATGAAAGTTTAAAGTGAGTTCAACATGATTT 40210
QY 361 AGTACCAATCAGATTTTATTCCTTCTTTGTATGAAACAAATGCTATTAAAT 420
DB 40211 AGTACCAATCAGATTTTATTCCTTCTTTGTATGAAACAAATGCTATTAAAT 40270
QY 421 GAAATATCAAAAGATATATCTTATTTAAATATTAATTAATGAATGAAATGA 480
DB 40271 GAAATATCAAAAGATATATCTTATTTAAATATTAATTAATGAATGAAATGA 40330
QY 481 GCTTATATCATATGATGTTTATCACTCAGAGTACGACGAAATTAACGATTA 540

DB 40331 GCTTATATCATATGATGTTTATCACTCAGAGTACGACGAAATTAACGATTA 40390
QY 541 ATCTTTATCTGATTAATTTGAAGACGTTTAGTCAAAAGTTAAATTAACGAAT 600
DB 40391 ATCTTTATCTGATTAATTTGAAGACGTTTAGTCAAAAGTTAAATTAACGA 40450
QY 601 TCATTAAGAAAGAAATTAATTTAATTTAAACAGAGATTTAAATGA 651
DB 40451 TCATTAAGAAAGAAATTAATTTAATTTAAACAGAGATTTAAATGA 40501

RESULT 3

AA68106 AAC68106 standard; cDNA; 41708 BP.

AC AAC68106;

DT 06-AUG-2003 (revised)

DT 29-AUG-2001 (first entry)

DE Complete genome of bacteriophage 77.

XX DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
XX screening assay; ss.

OS Bacteriophage.

XX WO200146383-A2.

PD 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US035180.

XX 22-DEC-1999; 99US-00470512.

PR 12-OCT-2000; 2000US-00689952.

XX (PHAG-) PHAGETECH INC.

PA (WILLI) WILLIAMS K M.

XX Pelletier J, Gros P, Dubow N;

PI WPI; 2001-418052/44.

XX Novel DnaI polypeptides useful for treating and diagnosing microbial,

PT preferably bacterial, diseases such as those caused by Staphylococcus

PT aureus.

XX Disclosure; Fig 2; 107pp; English.

XX This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcal, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for

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OM nucleic - nucleic search, using SW model

(without alignments)
6389.277 Million cell updates/sec

Perfect score: 651

651

Gapor 60.0 , Gapext 60.0

Total number of hits satisfying chosen parameters: 55026578

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 1000 summaries

Database :

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EST: +
1:  em_estba: +
2:  em_esthum:
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QY	1	ATGAAACAAGAAATATAGAAAGCATATATACCTTATAGCAAGAGGTGTCTCTTATTTCA	60
Ds	39851	ATGAAACAAGAAATATAGAAAGCATATATACCTTATAGCAAGAGGTGTCTCTTATTTCA	39910
QY	61	GTTAAAGATTTTACGATTTATTAACGATCTACCTACACGCTAAAAATATCATTTTA	120
Ds	39911	GTTAAAGATTTTACGATTTTATTTACGATCTACCTACACGCTAAAAATATCATTTTA	39970
QY	121	GAACAAAATATCCGATATATTTAGATGTGTTTTAAAAGGCTAAAAAGATGATGAGCT	180
Ds	39971	GAACAAAATATATCCGATATATTTAGATGTGTTTTAAAAGGCTAAAAAGATGATGAGCT	40030
QY	181	TATATTTATCCACAGAACGATGATTTTATGATTTTGTATGATGAGCTTTAAT	240
Ds	40031	TATATTTATCCACAGAACGATGATTTTATGATTTTGTATGATGAGCTTTAAT	40090
QY	241	AATTTAATATAGCAAAAGTAAAAAGCGTATGAAAATGTTATGATTTATGACAAATGAT	300
Ds	40091	AATTTAATATAGCAAAAGTAAAAAGCGTATGAAAATGTTATGATTTATGACAAATGAT	40150
QY	301	AATTTATCAATATAGGTTATGAGCAATGSAAGATTTTAAATAGAGTTTCAACATGAAAT	360
Ds	40151	AATTTATCAATATAGGTTATGAGCAATGSAAGATTTTAAATAGAGTTTCAACATGAAAT	40210
QY	361	AGTCAAAATCAGATTTTTTTAATCCTTCCTTGTATGSAACAAATGCTATTAATAT	420
Ds	40211	AGTCAAAATCAGATTTTTTTAATCCTTCCTTGTATGSAACAAATGCTATTAATAT	40270
QY	421	GAAATATCAAAAAGATATATCTATTTATAAAAATATAATTAATTAATGAATGAAAAATGA	480
Ds	40271	GAAATATCAAAAAGATATATCTATTTATAAAAATATAATTAATTAATGAATGAAAAATGA	40330
QY	481	GCTTATATCATATTTGATAGTTATATCATCTTCACAGTACCGACGAAAAATTAACGATAT	540
Ds	40331	GCTTATATCATATTTGATAGTTATATCATCTTCACAGTACCGACGAAAAATTAACGATAT	40390
QY	541	AATCTTATCTTGAATAATTTGAAGAACGTTTATGTCAAAAGTTTAAATTAACAGACT	600
Ds	40391	AATCTTATCTTGAATAATTTGAAGAACGTTTATGTCAAAAGTTTAAATTAACAGACT	40450
QY	601	TGCATTAAGAAAGATTAATTTAATTTAAACAAGAGAGATTTAAATGA	661
Ds	40451	TGCATTAAGAAAGATTAATTTAATTTAAACAAGAGAGATTTAAATGA	40501

Search completed: October 15, 2004, 00:15:51
Job time : 468.29 secs

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OM nucleic - nucleic search, using sw model

Run on:      October 14, 2004, 22:42:59 ; Search time 3042.64 Seconds
              (without alignments)
              6389,277 Million cell updates/second

Title:       US-09-407-804A-5
Perfect score: 651
Sequence:    1 atgaacgagcaataatag.....acaagagagatttaataga 651

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched:    27513289 seqs, 14931090276 residues

Word size :    0

Total number of hits satisfying chosen parameters:    55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :

EST:*
1:  em_estda:*
2:  em_esthum:*
3:  em_estln:*
4:  em_estnu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_hic:*
9:  gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mem:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_phg:*
27: em_gss_vrl:*

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28: gb_gses1:~
29: gb_gses2:~

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	3.7	471	29	AG243044	AG243044 Lotus cor
2	24	3.7	621	12	BH162873	BH162873 EST363396
3	24	3.7	688	29	CG185633	CG185633 PUICP69TD
4	24	3.7	824	28	B2728378	B2728378 OGEGR29TC
5	24	3.7	848	29	CG296548	CG296548 OGIBCI11TH
6	23	3.5	300	10	BF779194	BF779194 3106-34 h
7	23	3.5	596	29	CE154431	CE154431 t1gr-gsa-
8	22	3.4	443	28	A0036675	A0036675 CIT-HSP-2
9	22	3.4	495	28	A0598800	A0598800 HS_5338.B
10	22	3.4	531	12	BM273373	BM273373 PFE5T0a4
11	22	3.4	580	14	CD077038	CD077038 MA3-000IU
12	22	3.4	639	29	CG158238	CG158238 PUBB005TB
13	22	3.4	709	28	BH980591	BH980591 cda11504.
14	22	3.4	719	13	BK310093	BK310093 BX310093
15	22	3.4	745	28	CC166679	CC166679 1J85h10.9
16	22	3.4	757	12	BM170268	BM170268 EST572791
17	21	3.2	99	9	AA485711	AA485711 ab10504.s
18	21	3.2	190	9	A1688140	A1688140 w83310.x
19	21	3.2	205	12	BM666504	BM666504 UT-E-CQ1-
20	21	3.2	370	14	CB852711	CB852711 UT-CF-FNO
21	21	3.2	403	28	A0602480	A0602480 HS_2128.A
22	21	3.2	415	10	BE932045	BE932045 CM2-NT016
23	21	3.2	463	28	BE698220	BE698220 PUBWV41TD
24	21	3.2	463	28	BE701482	BE701482 PUBWV41TD
25	21	3.2	511	28	A0012488	A0012488 CIT-HSP-2
26	21	3.2	511	29	AG235001	AG235001 Lotus cor
27	21	3.2	660	29	BK167829	BK167829 Daulto rer
28	21	3.2	665	28	A2310475	A2310475 IM0025N23
29	21	3.2	673	29	AG036854	AG036854 Pan trogl
30	21	3.2	675	28	BH001460	BH001460 BMAC01B0
31	21	3.2	717	12	BM169216	BM169216 EST571739
32	21	3.2	717	12	BM940220	BM940220 UT-H-GCOP
33	21	3.2	735	29	CC866757	CC866757 ND1.13219
34	21	3.2	855	14	CD171657	CD171657 AGENCOURT
35	21	3.2	875	28	BH159742	BH159742 ENTRB76TR
36	21	3.2	891	13	BUI59551	BUI59551 AGENCOURT
37	21	3.2	891	29	CG114269	CG114269 PUBDC84TD
38	21	3.2	901	28	A2678579	A2678579 ENTRB22TR
39	21	3.2	939	28	BH134383	BH134383 ENTRC12TR
40	21	3.2	940	28	BH130856	BH130856 ENTRF60TR
41	21	3.2	948	29	CG114266	CG114266 PUBDC84TB
42	21	3.2	949	28	A2684730	A2684730 ENTRV47TF
43	21	3.2	1015	12	BM394551	BM394551 50072-2-4
44	21	3.2	1060	28	CC266828	CC266828 CH261-124
45	21	3.2	1064	29	CMS07B98	AL437586 T3 end of

c 103	20	3.1	496	9	AA910322	AA910322 ok83c03.s	c 160	20	3.1	708	13	BU687141
c 104	20	3.1	497	28	BH650569	BH650569 BOKCH21TF	c 161	20	3.1	712	9	AV854129
c 105	20	3.1	498	29	CCB60228	CCB60228 NDL.39D22	c 162	20	3.1	712	13	BU201985
c 106	20	3.1	503	14	CA266852	CA266852 SCNRJRT306	c 163	20	3.1	716	9	AV896978
c 107	20	3.1	516	28	AZ462156	AZ462156 1M0269M16	c 164	20	3.1	716	9	AV902615
c 108	20	3.1	517	9	AI581402	AI581402 t071e04.*	c 165	20	3.1	716	13	BO504920
c 109	20	3.1	521	12	BM275695	BM275695 PFEST0a5	c 166	20	3.1	719	13	BU292823
c 110	20	3.1	523	28	AQ370898	AQ370898 HS_3048_A	c 167	20	3.1	719	29	CE010772
c 111	20	3.1	524	10	AW514968	AW514968 xv01e01.x	c 168	20	3.1	721	14	CB241338
c 112	20	3.1	526	10	AW934532	AW934532 EST353436	c 169	20	3.1	721	28	AO578376
c 113	20	3.1	527	12	BG817799	BG817799 ESSU0221	c 170	20	3.1	722	14	CA438977
c 114	20	3.1	540	10	BF594507	BF594507 7b76a05.x	c 171	20	3.1	732	28	BZ500908
c 115	20	3.1	540	28	AO828809	AO828809 HS_5262_A	c 172	20	3.1	736	13	BU268247
c 116	20	3.1	546	12	BM671574	BM671574 UI-E-CQ1-	c 173	20	3.1	738	28	AO542040
c 117	20	3.1	560	12	BU415023	BU415023 BU415023	c 174	20	3.1	741	29	BX226352
c 118	20	3.1	562	12	BM452235	BM452235 K-EST0133	c 175	20	3.1	746	9	AV854153
c 119	20	3.1	564	29	CE785209	CE785209 t1qf-gs-	c 176	20	3.1	746	9	AV854165
c 120	20	3.1	581	10	B6673673	B6673673 7d79d02.x	c 177	20	3.1	749	13	BU351749
c 121	20	3.1	583	28	AZ977754	AZ977754 2M0253H15	c 178	20	3.1	772	13	BU331126
c 122	20	3.1	586	14	BZ150679	BZ150679 CH20-492	c 179	20	3.1	776	29	CCB96530
c 123	20	3.1	586	14	CB114682	CB114682 K-EST0158	c 180	20	3.1	779	28	BZ743489
c 124	20	3.1	587	12	BM726595	BM726595 UI-E-EJ0-	c 181	20	3.1	786	28	BZ787787
c 125	20	3.1	587	13	BU731541	BU731541 UI-E-C11-	c 182	20	3.1	798	12	BI489318
c 126	20	3.1	588	28	AO503855	AO503855 RPCI-11-3	c 183	20	3.1	801	28	BH115572
c 127	20	3.1	589	12	BG592540	BG592540 EST91218	c 184	20	3.1	816	28	BZ400834
c 128	20	3.1	590	12	BH127330	BH127330 1e97g08.x	c 185	20	3.1	816	28	BZ407739
c 129	20	3.1	594	12	BM681245	BM681245 UI-E-BJ0-	c 186	20	3.1	817	28	BH608020
c 130	20	3.1	602	29	CG277936	CG277936 OG0CC48TH	c 187	20	3.1	817	28	BZ407745
c 131	20	3.1	602	29	CG277948	CG277948 OG0CC48TV	c 188	20	3.1	823	28	BZ806722
c 132	20	3.1	605	9	AA552372	AA552372 nk13a08.s	c 189	20	3.1	824	28	AZ668681
c 133	20	3.1	607	9	AV903320	AV903320 AV903220	c 190	20	3.1	824	28	BH729885
c 134	20	3.1	607	28	CC313313	CC313313 TAM2-22C	c 191	20	3.1	829	12	BH500790
c 135	20	3.1	609	10	BF297344	BF297344 050PbE10	c 192	20	3.1	833	28	BH506755
c 136	20	3.1	617	28	AZ523869	AZ523869 224PB05	c 193	20	3.1	837	28	BH429914
c 137	20	3.1	625	14	CD717228	CD717228 VVB137A02	c 194	20	3.1	843	14	CB197584
c 138	20	3.1	633	28	BH764921	BH764921 BMBA0352E	c 195	20	3.1	844	28	BZ743479
c 139	20	3.1	645	12	BM786403	BM786403 K-EST0065	c 196	20	3.1	845	28	BZ168358
c 140	20	3.1	645	28	AQ324710	AQ324710 mgkA0019H	c 197	20	3.1	850	28	BH709588
c 141	20	3.1	648	10	BF296297	BF296297 035PB04	c 198	20	3.1	855	28	CC373920
c 142	20	3.1	652	28	BH177397	BH177397 009_M_15-	c 199	20	3.1	861	28	AO254724
c 143	20	3.1	652	29	CNS07079	AL614355 T3 end of	c 200	20	3.1	871	29	CG086792
c 144	20	3.1	655	12	BU411022	BU411022 BU411022	c 201	20	3.1	878	28	BZ396148
c 145	20	3.1	656	28	AZ362907	AZ362907 1M0108M08	c 202	20	3.1	881	28	AZ533488
c 146	20	3.1	656	28	AZ526470	AZ526470 255PBg11	c 203	20	3.1	882	29	CC713221
c 147	20	3.1	659	13	BU608492	BU608492 UI-CF-FN0	c 204	20	3.1	889	28	AZ674877
c 148	20	3.1	659	28	BZ954444	BZ954444 CH240_128	c 205	20	3.1	894	29	CG960947
c 149	20	3.1	663	12	BU415038	BU415038 BU415038	c 206	20	3.1	906	13	BU243888
c 150	20	3.1	665	29	CG794103	CG794103 ZMMBB031	c 207	20	3.1	912	28	BH135334
c 151	20	3.1	666	29	AG165507	AG165507 Pan tceq1	c 208	20	3.1	916	28	AZ689305
c 152	20	3.1	669	9	AV867854	AV867854 AV867854	c 209	20	3.1	916	28	BH147825
c 153	20	3.1	671	29	AG106328	AG106328 Pan tceq1	c 210	20	3.1	918	28	CD518168
c 154	20	3.1	677	10	BB612297	BB612297 BB612297	c 211	20	3.1	926	14	BO960665
c 155	20	3.1	677	10	BF295950	BF295950 032PB02	c 212	20	3.1	932	13	CG044639
c 156	20	3.1	680	29	AG153330	AG153330 Pan tceq1	c 213	20	3.1	941	29	CG955434
c 157	20	3.1	682	12	BM395300	BM395300 50072-2-8	c 214	20	3.1	954	29	CG955434
c 158	20	3.1	689	28	BH729537	BH729537 BOKKE53TF	c 215	20	3.1	984	29	CNS01VHY
c 159	20	3.1	694	28	BH932985	BH932985 od683e03.	c 216	20	3.1	988	29	CNS06GJ8

217	20	3.1	1044	13	B0884593	AGNOCOUNT	274	19	2.9	409	9	A1160741	A1160741	qP49d01.x
218	20	3.1	1101	29	CMS0505F		275	19	2.9	409	13	BW254872	BW254872	BW254872
219	20	3.1	1126	10	AA914486	EST345790	276	19	2.9	409	13	BK518203	BK518203	BK518203
220	20	3.1	1166	14	CD256342	AGNOCOUNT	277	19	2.9	411	9	A1825762	A1825762	A1825762
221	20	3.1	1176	13	B0836839	AGNOCOUNT	278	19	2.9	412	29	CE433057	CE433057	CE433057
222	19	2.9	123	10	AW898646	RCl-NN007	279	19	2.9	413	12	BG454241	BG454241	BG454241
223	19	2.9	124	29	BK662135	Arb4ldp25	280	19	2.9	414	10	B5668826	B5668826	B5668826
224	19	2.9	144	14	CF182010		281	19	2.9	414	9	A976542	A976542	A976542
225	19	2.9	156	10	B5520217		282	19	2.9	417	9	AU226809	AU226809	AU226809
226	19	2.9	177	29	CE626915	M11A10XTM	283	19	2.9	418	14	CA885168	CA885168	CA885168
227	19	2.9	208	9	AA963082	tiGr-gs+	284	19	2.9	418	14	CA885222	CA885222	CA885222
228	19	2.9	229	9	AA919428	vz19g09.r	285	19	2.9	419	10	BH711915	BH711915	BH711915
229	19	2.9	242	29	DR19E11T		286	19	2.9	420	10	AM344426	AM344426	AM344426
230	19	2.9	245	10	B8049312	reAr	287	19	2.9	424	14	CD422238	CD422238	CD422238
231	19	2.9	248	28	B2762639		288	19	2.9	424	14	CF927205	CF927205	CF927205
232	19	2.9	253	9	AV370356	SAIK.1060	289	19	2.9	424	28	A0698904	A0698904	A0698904
233	19	2.9	267	9	AV319318	AV319318	290	19	2.9	427	14	AA174512	AA174512	AA174512
234	19	2.9	276	9	AV220956		291	19	2.9	431	14	CF423619	CF423619	CF423619
235	19	2.9	278	14	R08997	R08997	292	19	2.9	431	14	CF423619	CF423619	CF423619
236	19	2.9	287	9	AV297852		293	19	2.9	433	14	CF428096	CF428096	CF428096
237	19	2.9	302	9	A1045061	UI-R-Cl-k	294	19	2.9	434	14	CF428096	CF428096	CF428096
238	19	2.9	307	12	BG945120		295	19	2.9	438	28	BH616043	BH616043	BH616043
239	19	2.9	309	14	CD586543		296	19	2.9	439	9	A1341579	A1341579	A1341579
240	19	2.9	313	13	BQ265314	NiSC.fT05	297	19	2.9	439	14	CD805622	CD805622	CD805622
241	19	2.9	317	14	CD524597	km09g11.y	298	19	2.9	441	28	A2685612	A2685612	A2685612
242	19	2.9	323	9	AA982864	ub59g03.r	299	19	2.9	443	10	BK030178	BK030178	BK030178
243	19	2.9	337	12	BP523862		300	19	2.9	442	14	CF805048	CF805048	CF805048
244	19	2.9	338	12	BG225761		301	19	2.9	444	14	CF835973	CF835973	CF835973
245	19	2.9	340	10	BF681900	6021177041	302	19	2.9	444	14	CF838491	CF838491	CF838491
246	19	2.9	342	10	BF134530	Uy16a12.y	303	19	2.9	446	9	AA887339	AA887339	AA887339
247	19</													

331	19	2.9	502	29	BX140474	Danlo_ref	388	19	2.9	597	28	BZ506214	BZ506214	BONEM61TF
332	19	2.9	503	9	A1788669	UK47H11.x	389	19	2.9	600	10	BF966137	BF966137	BZ506214
333	19	2.9	503	28	AQ157661	nbxb0009J	390	19	2.9	600	13	BU919204	BU919204	6014-89 M
334	19	2.9	505	14	CF599758	tac27602.	391	19	2.9	600	28	BZ401000	EINDRB6TF	BZ401000
335	19	2.9	509	9	AV523320	AV523320	392	19	2.9	601	28	AQ059872	CIT-HSP-2	AQ059872
336	19	2.9	509	12	BT745111	BT745111	393	19	2.9	602	13	BU307497	BU307497	601735480
337	19	2.9	512	14	NS4189	NS4189	394	19	2.9	604	14	CB400786	CB400786	OSTF182H6
338	19	2.9	515	10	BE370242	BE370242	395	19	2.9	607	9	AL969690	AL969690	AL969690
339	19	2.9	516	28	AQ776641	AQ776641	396	19	2.9	607	28	BZ403068	BZ403068	OGABJ04TM
340	19	2.9	517	10	AM696017	AM696017	397	19	2.9	607	29	CE492012	CE492012	CE492012
341	19	2.9	520	14	CF600262	CF600262	398	19	2.9	608	13	BU345563	BU345563	601522680
342	19	2.9	521	28	BZ859250	BZ859250	399	19	2.9	608	13	AQ0592162	AQ0592162	HS_3418_B
343	19	2.9	522	28	AZ851361	AZ851361	400	19	2.9	618	28	AQ156640	AQ156640	nbxb00080
344	19	2.9	523	10	AM691654	AM691654	401	19	2.9	622	13	BU607536	BU607536	UI-CF-FNO
345	19	2.9	523	12	AM6930136	AM6930136	402	19	2.9	630	28	BZ408277	BZ408277	OGAAV04TM
346	19	2.9	524	9	AL680061	AL680061	403	19	2.9	633	9	AV869625	AV869625	AV869625
347	19	2.9	525	29	CG407858	CG407858	404	19	2.9	633	28	BZ403058	BZ403058	OGABJ04TM
348	19	2.9	527	12	BM781214	BM781214	405	19	2.9	633	28	BZ408289	BZ408289	OGAAV04TM
349	19	2.9	527	14	CF116923	CF116923	406	19	2.9	637	13	CA051525	CA051525	OGAAV04TM
350	19	2.9	528	9	AM026438	AM026438	407	19	2.9	639	29	CE717429	CE717429	OGAAV04TM
351	19	2.9	528	29	CE736103	CE736103	408	19	2.9	640	10	BF308012	BF308012	601894280
352	19	2.9	530	28	AZ250223	AZ250223	409	19	2.9	642	14	CB442893	CB442893	693734_NA
353	19	2.9	535	9	AL960807	AL960807	410	19	2.9	643	13	BQ390010	BQ390010	NISC_mg10
354	19	2.9	536	10	AW120667	AW120667	411	19	2.9	644	10	BB630161	BB630161	BB630161
355	19	2.9	536	28	AZ283624	AZ283624	412	19	2.9	646	29	BX213184	BX213184	Danlo_ref
356	19	2.9	537	28	AQ438421	AQ438421	413	19	2.9	650	10	AM692470	AM692470	NF051125
357	19	2.9	539	10	BF062553	BF062553	414	19	2.9	650	14	CD598441	CD598441	RK114A1A0
358	19	2.9	540	29	CE365904	CE365904	415	19	2.9	651	28	BZ398417	BZ398417	EINBR6TF
359	19	2.9	545	9	AL594516	AL594516	416	19	2.9	658	10	AM691990	AM691990	OGAAV04TM
360	19	2.9	549	13	BK297104	BK297104	417	19	2.9	658	12	BG428656	BG428656	602494796
361	19	2.9	551	28	AZ740090	AZ740090	418	19	2.9	661	29	AG149784	AG149784	Pan_trog1
362	19	2.9	552	29	BX153265	BX153265	419	19	2.9	663	9	AU167028	AU167028	AU167028
363	19	2.9	553	10	BF057160	BF057160	420	19	2.9	663	28	BH673870	BH673870	BOKAB27TR
364	19	2.9	553	13	BQ451321	BQ451321	421	19	2.9	664	9	AL649832	AL649832	AL649832
365	19	2.9	562	28	AZ389303	AZ389303	422	19	2.9	664	28	BH482365	BH482365	BOPPC6TF
366	19	2.9	564	12	BI037229	BI037229	423	19	2.9	667	13	CA131564	CA131564	SCBGR104
367	19	2.9	565	28	BH664543	BH664543	424	19	2.9	668	29	CE197524	CE197524	CE197524
368	19	2.9	566	10	BE439425	BE439425	425	19	2.9	671	10	AM691359	AM691359	NF0468125
369	19	2.9	570	12	BG860408	BG860408	426	19	2.9	674	10	AM668672	AM668672	cdh66b08.
370	19	2.9	570	28	AQ768495	AQ768495	427	19	2.9	675	28	BH965397	BH965397	OGAAV04TM
371	19	2.9	571	28	BH716278	BH716278	428	19	2.9	676	9	AV649631	AV649631	AV649631
372	19	2.9	572	14	CD315332	CD315332	429	19	2.9	677	28	BH5197	BH5197	Pan_trog1
373	19	2.9	572	28	AQ959585	AQ959585	430	19	2.9	680	13	CA058064	CA058064	RFC111-30X3
374	19	2.9	574	14	CF360147	CF360147	431	19	2.9	680	29	CG796525	CG796525	CG796525
375	19	2.9	576	9	A1725746	A1725746	432	19	2.9	682	9	AV398127	AV398127	AV398127
376	19	2.9	580	28	BZ388361	BZ388361	433	19	2.9	682	9	BZ088561	BZ088561	1K88512.
377	19	2.9	585	28	BZ660251	BZ660251	434	19	2.9	684	28	BZ088561	BZ088561	OGABJ04TM
378	19	2.9	586	12	BM781057	BM781057	435	19	2.9	685	14	CB438449	CB438449	687052_NA
379	19	2.9	588	28	BZ915785	BZ915785	436	19	2.9	688	10	BF677499	BF677499	602085759
380	19	2.9	590	13	CA055901	CA055901	437	19	2.9	688	29	CA053077	CA053077	OGAAV04TM
381	19	2.9	591	29	DM16075	DM16075	438	19	2.9	689	28	AZ536836	AZ536836	Gm_15B001
382	19	2.9	594	10	AM636741	AM636741	439	19	2.9	689	28	AQ202318	AQ202318	RFC111-60
383	19	2.9	594	12	BG722571	BG722571	440	19	2.9	690	28	BZ498724	BZ498724	BONB23TR
384	19	2.9	596	13	BU579529	BU579529	441	19	2.9	691	14	CF206289	CF206289	RMR90915T
385	19	2.9	596	14	CP676675	CP676675	442	19	2.9	693	11	AY067503	AY067503	OGAAV04TM
386	19	2.9	597	10	BE204316	BE204316	443	19	2.9	700	13	BW148531	BW148531	OGAAV04TM
387	19	2.9	597	28	AZ855990	AZ855990	444	19	2.9	700	28	BZ398479	BZ398479	EINCR94TF

[illegible]

C 558	19	2.9	883	28	AZ671501	AZ671501	ENTLFB1TR	C 615	18	2.8	163	9	A1272046	A1272046	qj89b06.x
C 559	19	2.9	885	29	CG037742	CG037742	PURBEB3STD	C 616	18	2.8	163	29	CE704180	CE704180	t1qr-gsa-
C 560	19	2.9	885	29	CG455982	CG455982	PUIR293TD	C 617	18	2.8	164	28	BH908945	BH908945	SALK_0514
C 561	19	2.9	886	29	CG824097	CG824097	SOYDL65TH	C 618	18	2.8	168	9	AV547745	AV547745	AV547745
C 562	19	2.9	886	29	CG929375	CG929375	MBEMG3TF	C 619	18	2.8	177	9	AV418783	AV418783	AV418783
C 563	19	2.9	889	29	CG210355	CG210355	OG3CA75TV	C 620	18	2.8	179	12	BG587876	BG587876	AV418783
C 564	19	2.9	889	29	CG245747	CG245747	OG3AJ08TH	C 621	18	2.8	180	9	AV317644	AV317644	AV317644
C 565	19	2.9	890	28	AQ746296	AQ746296	HS_2277_A	C 622	18	2.8	190	10	AV197509	AV197509	AV197509
C 566	19	2.9	891	13	BK846462	BK846462	BH52191	C 623	18	2.8	195	9	AA050595	AA050595	AA050595
C 567	19	2.9	894	28	BH152191	BH152191	ENTPMO3TR	C 624	18	2.8	196	9	A1817602	A1817602	A1817602
C 568	19	2.9	895	29	CG771183	CG771183	TCB47_2_B	C 625	18	2.8	197	10	AW739699	AW739699	AW739699
C 569	19	2.9	906	28	BK846733	BK846733	ENTMOC6TF	C 626	18	2.8	213	9	A1523405	A1523405	A1523405
C 570	19	2.9	906	28	BH134935	BH134935	ENTMOC6TF	C 627	18	2.8	213	10	BH062035	BH062035	BH062035
C 571	19	2.9	908	13	BK329964	BK329964	BX329964	C 628	18	2.8	214	28	AZ820844	AZ820844	AZ820844
C 572	19	2.9	908	14	CGD27992	CGD27992	AGENCOURT	C 629	18	2.8	216	10	BF907394	BF907394	BF907394
C 573	19	2.9	909	14	CA280510	CA280510	SCVFL1CI	C 630	18	2.8	222	9	AV368716	AV368716	AV368716
C 574	19	2.9	910	29	CG929348	CG929348	MBEMD02TR	C 631	18	2.8	223	10	BB421704	BB421704	BB421704
C 575	19	2.9	911	28	AZ527591	AZ527591	ENTBH92TR	C 632	18	2.8	236	10	BB214458	BB214458	BB214458
C 576	19	2.9	912	28	AZ682943	AZ682943	ENTLCT4TF	C 633	18	2.8	239	10	BB169342	BB169342	BB169342
C 577	19	2.9	916	28	CG215347	CG215347	CH261-771	C 634	18	2.8	240	9	AU071754	AU071754	AU071754
C 578	19	2.9	919	14	CA793165	CA793165	AGENCOURT	C 635	18	2.8	240	9	AU074775	AU074775	AU074775
C 579	19	2.9	921	29	CG134308	CG134308	ENTGV20TF	C 636	18	2.8	242	14	CG367726	CG367726	CG367726
C 580	19	2.9	922	28	AZ668004	AZ668004	PUP0871TD	C 637	18	2.8	248	10	BB074631	BB074631	BB074631
C 581	19	2.9	928	28	BH164132	BH164132	ENTSH39TR	C 638	18	2.8	248	29	BK658660	BK658660	BK658660
C 582	19	2.9	932	29	CG174892	CG174892	PUIHLS1TD	C 639	18	2.8	250	14	CG047966	CG047966	CG047966
C 583	19	2.9	935	13	BH449888	BH449888	603215523	C 640	18	2.8	251	9	A1581616	A1581616	A1581616
C 584	19	2.9	935	29	CG351413	CG351413	OGOCCT5TH	C 641	18	2.8	254	28	BH183055	BH183055	BH183055
C 585	19	2.9	940	29	CG343898	CG343898	OGD0077TH	C 642	18	2.8	254	29	CNS07088	CNS07088	CNS07088
C 586	19	2.9	946	28	CG381083	CG381083	PURHRO5TD	C 643	18	2.8	256	29	CE038455	CE038455	CE038455
C 587	19	2.9	961	13	BH916400	BH916400	AGENCOURT	C 644	18	2.8	257	28	BZ961088	BZ961088	BZ961088
C 588	19	2.9	965	29	CG866382	CG866382	NDL_108M1	C 645	18	2.8	266	10	BB177775	BB177775	BB177775
C 589	19	2.9	968	29	CG351420	CG351420	OGOCCT5TV	C 646	18	2.8	266	14	T72567	T72567	T72567
C 590	19	2.9	968	13	BY18203	BY18203	CG148997	C 647	18	2.8	266	10	BE509036	BE509036	BE509036
C 591	19	2.9	978	29	CG149997	CG149997	PUPFH28TB	C 648	18	2.8	274	10	BE509036	BE509036	BE509036
C 592	19	2.9	1003	13	BH913308	BH913308	AGENCOURT	C 649	18	2.8	282	9	A1204402	A1204402	A1204402
C 593	19	2.9	1010	28	BZ610671	BZ610671	WHAC101TF	C 650	18	2.8	282	9	A1204402	A1204402	A1204402
C 594	19	2.9	1013	10	BE420876	BE420876	HMMO03_ED	C 651	18	2.8	282	12	BE092791	BE092791	BE092791
C 595	19	2.9	1014	29	CG149999	CG149999	PUPFH28TD	C 652	18	2.8	282	12	BE092791	BE092791	BE092791
C 596	19	2.9	1017	29	CNS01003	CNS01003	Drosoph11	C 653	18	2.8	283	10	BB366758	BB366758	BB366758
C 597	19	2.9	1027	28	CG278079	CG278079	CH261-151	C 654	18	2.8	286	10	BB264158	BB264158	BB264158
C 598	19	2.9	1057	28	BZ456057	BZ456057	BONKNS5TR	C 655	18	2.8	286	14	N90549	N90549	N90549
C 599	19	2.9	1075	28	BH684779	BH684779	BOKMG71TR	C 656	18	2.8	290	9	AV035896	AV035896	AV035896
C 600	19	2.9	1075	28	BZ456050	BZ456050	BONKNS5TF	C 657	18	2.8	291	9	A1263007	A1263007	A1263007
C 601	19	2.9	1101	13	BK327951	BK327951	BX327951	C 658	18	2.8	292	10	BB384163	BB384163	BB384163
C 602	19	2.9	1109	28	BZ392216	BZ392216	ELINCN19TR	C 659	18	2.8	293	12	BJ399468	BJ399468	BJ399468
C 603	19	2.9	1135	28	CG234931	CG234931	CH261-80J	C 660	18	2.8	293	28	CC124410	CC124410	CC124410
C 604	19	2.9	1159	28	CG291311	CG291311	CH261-94K	C 661	18	2.8	293	29	CC679976	CC679976	CC679976
C 605	19	2.9	1165	13	BH422983	BH422983	603953683	C 662	18	2.8	293	10	BB504221	BB504221	BB504221
C 606	19	2.9	1195	28	CG221535	CG221535	CH261-99K	C 663	18	2.8	295	10	BB487578	BB487578	BB487578
C 607	19	2.9	1229	28	CG282083	CG282083	CH261-158	C 664	18	2.8	295	28	AZ005920	AZ005920	AZ005920
C 608	19	2.9	1440	29	AG028206	AG028206	Pan tregl	C 665	18	2.8	299	10	AM415628	AM415628	AM415628
C 609	19	2.9	1447	11	AK01085	AK01085	Mus muscu	C 666	18	2.8	301	10	BB107767	BB107767	BB107767
C 610	19	2.9	2973	11	AK037072	AK037072	Mus muscu	C 667	18	2.8	301	14	N70978	N70978	N70978
C 611	18	2.8	1063	29	CNS01UID	CNS01UID	Tetradon	C 668	18	2.8	306	14	CE262778	CE262778	CE262778
C 612	18	2.8	106	13	BH887988	BH887988	P002806_P	C 669	18	2.8	306	29	CG930349	CG930349	CG930349
C 613	18	2.8	137	14	CA380342	CA380342	659611_NC	C 670	18	2.8	307	29	CE702960	CE702960	CE702960
C 614	18	2.8	138	13	BK251982	BK251982	BK251982	C 671	18	2.8	309	9	AA813553	AA813553	AA813553

c 672	18	2.8	309	10	BB393063	BB393063	c 729	18	2.8	376	9	AA454370	AA454370	MBACXKGO	
c 673	18	2.8	310	9	AI700142	AI700142 tq21a04.x	c 730	18	2.8	377	9	AA644458	AA644458	zU85f06.s	
c 674	18	2.8	310	14	CE287632	CE287632 ES7550354	c 731	18	2.8	377	10	BB332653	BB332653	BB332653	
c 675	18	2.8	310	29	CG020711	CG020711 ZMMBC055	c 732	18	2.8	378	12	BI332167	BI332167	k417b06.y	
c 676	18	2.8	311	10	BB272130	BB272130 BB272130	c 733	18	2.8	378	14	CK293889	CK293889	ES755613	
c 677	18	2.8	311	12	BM162016	BM162016 ES75564539	c 734	18	2.8	379	14	CK330789	CK330789	CG306H04-	
c 678	18	2.8	311	13	BO610633	BO610633 sap48f08.	c 735	18	2.8	381	29	CC793525	CC793525	SLAK_0153	
c 679	18	2.8	313	29	CG287425	CG287425 OGBK93TH	c 736	18	2.8	382	29	CG376370	CG376370	OGVDB28TH	
c 680	18	2.8	314	9	AV148267	AV148267 AV148267	c 737	18	2.8	383	9	AV524319	AV524319	AV524319	
c 681	18	2.8	314	10	BB119135	BB119135 BB119135	c 738	18	2.8	384	12	BG234590	BG234590	d4b67a10.	
c 682	18	2.8	314	28	AZ755645	AZ755645 ev02e06.x	c 739	18	2.8	386	9	AI630945	AI630945	ty99g02.x	
c 683	18	2.8	316	10	BB215221	BB215221 BB215221	c 740	18	2.8	387	9	AI554356	AI554356	q161e03.x	
c 684	18	2.8	316	12	BI497378	BI497378 df135f03.	c 741	18	2.8	388	12	BI050763	BI050763	RC6-GN007	
c 685	18	2.8	316	28	AQ236494	AQ236494 HS_2033_B	c 742	18	2.8	389	28	AQ217203	AQ217203	HS_2139_A	
c 686	18	2.8	317	29	BS08327	BS08327 dc10c10.x	c 743	18	2.8	391	9	AU087559	AU087559	AU087559	
c 687	18	2.8	317	29	AG264020	AG264020 Lotus cor	c 744	18	2.8	392	9	AI417873	AI417873	Q72d03.x	
c 688	18	2.8	318	9	AM072966	AM072966 na43d03.x	c 745	18	2.8	393	13	BX524438	BX524438	BX524438	
c 689	18	2.8	318	12	BM149575	BM149575 TCAP3D12	c 746	18	2.8	395	29	CE315286	CE315286	tl6T-gsa-	
c 690	18	2.8	318	28	AQ423026	AQ423026 CTBT-EI-	c 747	18	2.8	396	9	AI016653	AI016653	ou96a03.x	
c 691	18	2.8	322	9	AA335842	AA335842 EST40318	c 748	18	2.8	396	14	CF081B86	CF081B86	QHL14K23.	
c 692	18	2.8	324	10	AM768321	AM768321 hk39g04.x	c 749	18	2.8	396	14	N71037	N71037	za35a06.s1	
c 693	18	2.8	324	10	BB085173	BB085173 BB085173	c 750	18	2.8	398	29	CC466910	CC466910	CH240_136	
c 694	18	2.8	325	28	BZ192929	BZ192929 CH230-279	c 751	18	2.8	399	14	T85387	T85387	yd76a02.r1	
c 695	18	2.8	326	28	BZ056796	BZ056796 BOMNT49TF	c 752	18	2.8	400	9	AI973147	AI973147	wF5Db07.x	
c 696	18	2.8	329	13	BQ253787	BQ253787 san67b10.	c 753	18	2.8	400	13	BI574572	BI574572	BYS74572	
c 697	18	2.8	332	9	AA497251	AA497251 fa03h10.s	c 754	18	2.8	400	14	W80609	W80609	z482a11.s1	
c 698	18	2.8	332	10	BB780287	BB780287 BB780287	c 755	18	2.8	404	9	AI540307	AI540307	CG292876	
c 699	18	2.8	333	12	BI742418	BI742418 kt50e12.y	c 756	18	2.8	404	14	CK292876	CK292876	ES755590	
c 700	18	2.8	334	12	BG626293	BG626293 CC-esf1CL	c 757	18	2.8	405	9	AA809630	AA809630	nz17h01.s	
c 701	18	2.8	335	13	BK679866	BK679866 BX679866	c 758	18	2.8	405	14	AA814857	AA814857	AV814857	
c 702	18	2.8	336	9	AU267023	AU267023 AU267023	c 759	18	2.8	406	28	BZ761419	BZ761419	SAUK_0004	
c 703	18	2.8	336	14	CF807601	CF807601 p3HB026xE	c 760	18	2.8	410	14	CB804014	CB804014	AMGRN0C:S	
c 704	18	2.8	337	9	AL389348	AL389348 mCB54C08	c 761	18	2.8	411	12	BM122223	BM122223	L0507B09-	
c 705	18	2.8	341	9	AI000490	AI000490 cs95b01.s	c 762	18	2.8	411	28	AZ756397	AZ756397	ev07c07.r	
c 706	18	2.8	346	10	AM628526	AM628526 h138d06.x	c 763	18	2.8	412	12	BM724754	BM724754	ev14a02.r	
c 707	18	2.8	347	9	AI493003	AI493003 g247f03.x	c 764	18	2.8	412	13	BQ090846	BQ090846	U1-E-BU0-	
c 708	18	2.8	347	9	AL272916	AL272916 AL272916	c 765	18	2.8	412	12	AZ756617	AZ756617	ku21a08.y	
c 709	18	2.8	350	14	CF504520	CF504520 USDX-FP_1	c 766	18	2.8	412	14	BT79553	BT79553	yd75f02.r1	
c 710	18	2.8	352	9	AA415199	AA415199 vc9Bb03.s	c 767	18	2.8	412	13	BQ090846	BQ090846	tl6T-gsa-	
c 711	18	2.8	355	9	AI139435	AI139435 qc20e01.x	c 768	18	2.8	413	29	CE474335	CE474335	tl6T-gsa-	
c 712	18	2.8	355	14	CD450479	CD450479 USDX-FP_1	c 769	18	2.8	414	28	AQ355829	AQ355829	CTBT-EI-	
c 713	18	2.8	355	28	AZ755639	AZ755639 ev02d11.x	c 770	18	2.8	415	9	AI381523	AI381523	ev07c07.r	
c 714	18	2.8	356	12	BP432166	BP432166 BP432166	c 771	18	2.8	417	10	BF875164	BF875164	QV3-E7010	
c 715	18	2.8	356	13	BI340756	BI340756 BI340756	c 772	18	2.8	418	28	AZ254394	AZ254394	Gm_UMp001	
c 716	18	2.8	357	10	AM530473	AM530473 UI-R-C4-a	c 773	18	2.8	418	28	BM744310	BM744310	gt35d03.b	
c 717	18	2.8	362	14	CD421256	CD421256 ku81d09.y	c 774	18	2.8	419	29	CE799498	CE799498	tl6T-gsa-	
c 718	18	2.8	363	9	AI081817	AI081817 ck77f10.x	c 775	18	2.8	420	9	AI039024	AI039024	ox10a05.s	
c 719	18	2.8	364	28	CC199671	CC199671 XH623 Bay	c 776	18	2.8	421	14	CB506659	CB506659	ss41cnd01	
c 720	18	2.8	367	9	AI784856	AI784856 SWANCA30	c 777	18	2.8	421	28	AQ684922	AQ684922	HS_2147_A	
c 721	18	2.8	369	10	BF469524	BF469524 UI-N-BH3-	c 778	18	2.8	421	29	CE824584	CE824584	tl6T-gsa-	
c 722	18	2.8	372	9	AA652550	AA652550 na72e11.s	c 779	18	2.8	422	9	AA779505	AA779505	af23f01.s	
c 723	18	2.8	372	14	W23402	W23402 RRMCAL2885	c 780	18	2.8	422	12	AI040795	AI040795	cx10a05.s	
c 724	18	2.8	372	28	BM334402	BM334402 CH230-202	c 781	18	2.8	424	14	BI881766	BI881766	fn07c03.x	
c 725	18	2.8	373	9	AU267305	AU267305 AU267305	c 782	18	2.8	424	14	N66061	N66061	z429e03.s1	
c 726	18	2.8	374	28	AQ218662	AQ218662 HS_3245_B	c 783	18	2.8	424	28	AQ771938	AQ771938	HS_5397_B	
c 727	18	2.8					c 784	18	2.8						
c 728	18	2.8					c 785	18	2.8	425	9	AI089763	AI089763	qa22e09.x	

786	18	2.8	425	28	BB7014	BB7014 RPL11-26P2	843	18	2.8	465	10	BB831573
787	18	2.8	426	10	BB825933	BB825933 BB825933	844	18	2.8	466	9	AI522285
788	18	2.8	426	12	BM128447	BM128447 I f14h01.x	845	18	2.8	467	9	AA564113
789	18	2.8	426	14	CB695586	CB695586 AMGNHC:T	846	18	2.8	468	28	BH325270
790	18	2.8	427	9	AI741708	AI741708 wg22608.x	847	18	2.8	471	10	AM953277
791	18	2.8	427	14	HS8603	HS8603 yr06a10.-s1	848	18	2.8	472	9	AA677563
792	18	2.8	428	9	AM069332	AM069332 ct44d01.x	849	18	2.8	472	14	CM267554
793	18	2.8	429	9	AA873867	AA873867 ds34d09.s	850	18	2.8	473	14	CM544022
794	18	2.8	430	9	AI566849	AI566849 tm24c09.x	851	18	2.8	474	9	AI043035
795	18	2.8	430	28	AQ114645	AQ114645 CIT-HSP-2	852	18	2.8	474	28	AZ742274
796	18	2.8	431	9	AI361766	AI361766 wt67c09.x	853	18	2.8	474	28	BZ342982
797	18	2.8	431	28	AA0838427	AA0838427 HS_5175_B	854	18	2.8	474	29	CG199408
798	18	2.8	432	9	AI689917	AI689917 mm63f04.x	855	18	2.8	475	9	AI164422
799	18	2.8	432	12	BM069826	BM069826 Ie90e04.y	856	18	2.8	475	10	BE685868
800	18	2.8	432	28	BH521887	BH521887 BOHCGO9TR	857	18	2.8	476	13	BU632377
801	18	2.8	433	12	BP126442	BP126442 BP126442	858	18	2.8	476	29	AG250282
802	18	2.8	435	12	BM461655	BM461655 A00940-R	859	18	2.8	477	10	BM992962
803	18	2.8	435	13	BQ426363	BQ426363 CgHem_012	860	18	2.8	477	13	BQ426826
804	18	2.8	436	28	BE761409	BE761409 SALX_0003	861	18	2.8	479	29	CE526721
805	18	2.8	436	9	AI206106	AI206106 qg28c11.x	862	18	2.8	479	29	CG199411
806	18	2.8	436	28	AA513425	AA513425 HS_5144_A	863	18	2.8	480	12	BG276587
807	18	2.8	437	9	AI709276	AI709276 aa63c04.x	864	18	2.8	481	9	AU274955
808	18	2.8	438	9	AA991188	AA991188 ca24e12.s	865	18	2.8	481	28	AQ286172
809	18	2.8	438	9	AI105306	AI105306 EST214595	866	18	2.8	481	28	BH828712
810	18	2.8	438	14	CD764696	CD764696 GGEZL101	867	18	2.8	481	28	BH828712
811	18	2.8	438	14	R98307	R98307 yr30g04.f1	868	18	2.8	482	9	AM044322
812	18	2.8	441	14	CD421495	CD421495 Ku84h11.y	869	18	2.8	482	28	AA550085
813	18	2.8	442	9	AI076460	AI076460 oz17d08.x	870	18	2.8	483	9	AI660143
814	18	2.8	442	13	BQ615134	BQ615134 fmb22f04.	871	18	2.8	485	9	AI942957
815	18	2.8	445	28	AZ587222	AZ587222 IM0394N12	872	18	2.8	485	28	BE2831863
816	18	2.8	445	29	CNS06C08	AI392696.f77 end of	873	18	2.8	486	13	BK681490
817	18	2.8	446	9	AI494602	AI494602 qe01h03.x	874	18	2.8	488	9	AU289792
818	18	2.8	446	10	AM82623	AM82623 ua19g07.y	875	18	2.8	489	10	BE604618
819	18	2.8	446	13	BX102006	BX102006 BX102006	876	18	2.8	489	14	CA662502
820	18	2.8	447	9	AI360740	AI360740 qy05e08.x	877	18	2.8	491	28	AQ040657
821	18	2.8	447	14	CB746483	CB746483 AMGNHC:M	878	18	2.8	491	28	BX122318
822	18	2.8	448	9	AI628401	AI628401 ty76a10.x	879	18	2.8	492	9	AI002164
823	18	2.8	449	9	AI167417	AI167417 oa69h02.s	880	18	2.8	492	28	AQ977034
824	18	2.8	450	13	BM027777	BM027777 BM027777	881	18	2.8	492	28	BZ481582
825	18	2.8	450	28	B526539	B526539 OGAH150TC	882	18	2.8	493	28	B34104
826	18	2.8	451	9	AU264546	AU264546 AU264546	883	18	2.8	493	14	CD855688
827	18	2.8	451	9	AM084654	AM084654 ka45h07.x	884	18	2.8	495	14	CD855688
828	18	2.8	451	14	CD184652	CD184652 MSI-00496	885	18	2.8	495	28	AQ507196
829	18	2.8	453	14	CD685576	CD685576 EST2097.h	886	18	2.8	496	10	BE473338
830	18	2.8	454	28	BH248786	BH248786 PSB1357.1	887	18	2.8	496	14	234011
831	18	2.8	455	13	BY691997	BY691997 BY691997	888	18	2.8	496	28	AQ063790
832	18	2.8	456	10	BE579332	BE579332 kg2e06.y	889	18	2.8	497	28	AQ450035
833	18	2.8	456	10	BE950189	BE950189 UI-W-CEO-	890	18	2.8	497	29	CE689547
834	18	2.8	457	9	AI657394	AI657394 w155f04.x	891	18	2.8	498	9	AA481187
835	18	2.8	457	14	CD452309	CD452309 USDH-FP_1	892	18	2.8	498	12	BG638581
836	18	2.8	461	9	AI276516	AI276516 q176g12.x	893	18	2.8	498	13	BY616789
837	18	2.8	461	10	BE209379	BE209379 so27c06.y	894	18	2.8	499	13	BQ426930
838	18	2.8	461	29	CNS06C0P	AI396527.T3 end of	895	18	2.8	499	13	BQ427291
839	18	2.8	462	10	BB633901	BB633901 BB633901	896	18	2.8	500	9	AI418960
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841	18	2.8	464	9	AI477037	AI477037 fb34h07.x	898	18	2.8	500	13	BQ426831
842	18	2.8	464	9	AA244720	AA244720 mx31h11.r	899	18	2.8	500	28	AQ003180

c 900	18	2.8	500	28	BH892508	3526.1_21	957	18	2.8	549	29	CE460344	CE460344	tigr-gss-
501	18	2.8	501	12	BH287116	527399_MA	c 958	18	2.8	549	29	CE779393	CE779393	tigr-gss-
502	18	2.8	503	9	AL706536	DKEP2666H	959	18	2.8	550	14	CD372362	CD372362	UI-R-G00-
c 903	18	2.8	504	14	CF428756	1ad43h02.	c 960	18	2.8	551	13	BX58091	BX58091	BM58091
c 904	18	2.8	504	28	AA060067	CIT-HSP-2	c 961	18	2.8	551	14	BM053049	BM053049	NISC-g706
c 905	18	2.8	505	9	AA395681	28083_Lam	c 962	18	2.8	552	12	BM053049	BM053049	1669f05.y
c 906	18	2.8	506	13	BQ426988	Cyhem 017	c 963	18	2.8	552	14	CB428711	CB428711	604456_MA
c 907	18	2.8	506	28	BH178383	BH178383_011_B_02-	c 964	18	2.8	552	28	CC070819	CC070819	CSU-K331-
c 908	18	2.8	506	28	BZ304999	AL615340_T3_end_of	c 965	18	2.8	554	29	CE367929	CE367929	tigr-gss-
c 909	18	2.8	506	29	CNS07KPM	BE002904_OVA-BN009	c 966	18	2.8	554	29	CE383824	CE383824	tigr-gss-
c 910	18	2.8	508	10	BE002904	BH366037_603788879	c 967	18	2.8	555	9	A1721681	A1721681	fc30h11.x
c 911	18	2.8	509	13	BU366037	BZ960530_PUGFO66TB	c 968	18	2.8	555	28	BH891811	BH891811	3526.1_19
c 912	18	2.8	509	28	BZ960530	BH207094_Sm-52EL1	c 969	18	2.8	557	12	BI594812	BI594812	As_tg2_44
c 913	18	2.8	511	28	BH207094	AI999076_701517060	c 970	18	2.8	559	12	BP523715	BP523715	BP523715
c 914	18	2.8	515	9	A1999076	BM274588_BW274588	c 971	18	2.8	561	14	CA418736	CA418736	UI-H-E21-
c 915	18	2.8	515	14	CD700802	BM274588_BW274588	c 972	18	2.8	562	14	CA418736	CA418736	UI-H-E21-
c 916	18	2.8	516	13	BM274588	BX549386_BX549386	c 973	18	2.8	563	12	BM276540	BM276540	Lotus cor
c 917	18	2.8	516	13	BX549386	AO622463_HS_2085_A	c 974	18	2.8	563	12	AZ2259308	AZ2259308	PFS00a48
c 918	18	2.8	517	28	AO622463	BY480600_BY480600	c 975	18	2.8	563	28	BH315641	BH315641	BJ081706
c 919	18	2.8	517	13	BY480600	CE294483_EST757197	c 976	18	2.8	564	12	BJ081706	BJ081706	StrPu538.
c 920	18	2.8	518	14	CK294483	A2929048_479_d1f21	c 977	18	2.8	564	28	BH869266	BH869266	h143b11.g
c 921	18	2.8	518	28	A2929048	B2501471_BONQF6TF	c 978	18	2.8	564	28	BH869266	BH869266	h143b11.g
c 922	18	2.8	518	28	B2501471	AI675577_wc21d08.x	c 979	18	2.8	565	29	CE654583	CE654583	tigr-gss-
c 923	18	2.8	519	9	A1675577	BP181726_BP181726	c 980	18	2.8	565	9	AL694074	AL694074	DKEP313C
924	18	2.8	521	12	BP181726	BX085782_BX085782	c 981	18	2.8	565	13	BX38599	BX38599	BX38599
925	18	2.8	522	13	BX085782	AL176944_SP_0145_A	c 982	18	2.8	565	28	BH764595	BH764595	BMBAC350F
926	18	2.8	522	28	AL176944	BH891734_3526.1_19	c 983	18	2.8	566	14	CB534676	CB534676	768029_MA
c 927	18	2.8	524	28	BH891734	CE693359_SP_Ba003	c 984	18	2.8	569	28	BZ687417	BZ687417	PUBBH71TD
928	18	2.8	524	28	BZ693359	CE302058_tigr-gss-	c 985	18	2.8	569	29	AG240999	AG240999	Lotus cor
929	18	2.8	524	29	CE302058	CE246361_tigr-gss-	c 986	18	2.8	570	10	AM872021	AM872021	da86602.y
930	18	2.8	525	13	CE246361	BX532233_BX532233	c 987	18	2.8	572	29	CC845239	CC845239	NDL_87E3.
c 931	18	2.8	526	13	BX532233	A2526524_256Pb012	c 988	18	2.8	573	13	BQ384980	BQ384980	NISC_m010
c 932	18	2.8	527	28	A2526524	CA203097_SCAGFL109	c 989	18	2.8	573	13	CA046490	CA046490	ssalBrh01
933	18	2.8	528	14	CA203097	AO876515_HS_5298_A	c 990	18	2.8	573	29	CG984068	CG984068	CH240_153
c 934	18	2.8	529	28	AO876515	AZ486212_1M0314N02	c 991	18	2.8	575	28	AZ820852	AZ820852	ZM0033P14
c 935	18	2.8	529	28	AZ486212	BZ405101_OGAP547C	c 992	18	2.8	575	28	BH331918	BH331918	CH230-125
c 936	18	2.8	530	9	A1983933	AA482495_zv29e05.s	c 993	18	2.8	576	12	BM087257	BM087257	499960_MA
c 937	18	2.8	530	9	AA482495	BX569085_BX569085	c 994	18	2.8	576	12	BM087257	BM087257	499960_MA
c 938	18	2.8	530	13	BX569085	BH891822_3526.1_19	c 995	18	2.8	577	28	BZ940807	BZ940807	CH240_90H
c 939	18	2.8	530	28	BH891822	BX561545_BX561545	c 996	18	2.8	578	9	AV674409	AV674409	PFS00a48
c 940	18	2.8	533	12	BX561545	CD756584_AGENCOURT	c 997	18	2.8	578	12	BI667453	BI667453	ft54h12.x
c 941	18	2.8	536	14	CD756584	BZ938838_CH240_105	c 998	18	2.8	580	14	CD250537	CD250537	StrPu691.
c 942	18	2.8	537	28	BZ938838	BG994419_PMO-HT091	c 999	18	2.8	581	9	AU033718	AU033718	NU033718
c 943	18	2.8	538	12	BG994419	AO474226_CITBI-E1-	c 1000	18	2.8	581	9	AU033718	AU033718	NU033718
c 944	18	2.8	538	12	BI678751	BI678751_SWS590_SW								
c 945	18	2.8	538	12	BI678751	AO474226_CITBI-E1-								
c 946	18	2.8	539	12	BI678751	BI678751_SWS590_SW								
c 947	18	2.8	539	12	BI678751	AO504220_RPCI-11-2								
c 948	18	2.8	539	12	BI678751	AO504220_RPCI-11-2								
c 949	18	2.8	540	28	AO504220	AO417782_RPCI-11-2								
950	18	2.8	541	29	AO504220	AI735498_Arbd10ps								
c 951	18	2.8	544	29	AO504220	AA699466_t143d06.s								
c 952	18	2.8	545	9	AA699466	AA699466_t143d06.s								
c 953	18	2.8	545	9	AA699466	AO376974_RPCI11-16								
c 954	18	2.8	545	28	AO376974	AO376974_RPCI11-16								
c 955	18	2.8	546	13	BX250549	BX250549_NXNV045_F								
c 956	18	2.8	549	28	BX250549	AZ334599_1M0093123								

ALIGNMENTS

AG243044/c	471 bp	DNA	linear	GSS 19-JUL-2003
LOCUS	AG243044			
DEFINITION	Lotus corculiculatus var. japonicus DNA, clone:ljt12a08_not, genomic			
survey sequence.				
ACCESSION	AG243044			
VERSION	AG243044.1			
KEYWORDS	GSS.			
	GT:26642809			

SOURCE
Lotus corniculatus var. japonicus (Lotus japonicus)

ORGANISM
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;
Lotus.

REFERENCE
1
Sato, S., Nakamura, Y. and Tsubate, S.

AUTHORS
Lotus japonicus TAC End sequences

JOURNAL
Published Only in Database (2002)

REFERENCE
2 (bases 1 to 471)

AUTHORS
Sato, S.

TITLE
Direct Submision

JOURNAL
Submitted (20-NOV-2002) Shusui Sato, Kazusa DNA Research Institute,
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Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: sato@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)

FEATURES
Location/Qualifiers
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/organism="Lotus corniculatus var. japonicus"
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/variety="japonicus"
/db_xref="taxon:34305"
/clone="LJ12a08_not"
/clone_1db="genomic TAC library"
/note="VECTOR: pYLINACT-synonym: Lotus japonicus"

ORIGIN
Query Match 3.7%; Score 24; DB 29; Length 471;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 TATATTAATTAATGAATGAAAA 476
|||||
211 TATATTAATTAATGAATGAAAA 188

Db

RESULT 2
BM162873 621 bp mRNA linear EST 04-DEC-2001
LOCUS EST563396 PyBS Plasmodium yoelii yoelii cDNA clone PYCRX03 5' end,
DEFINITION mRNA sequence.
ACCESSION BM162873
VERSION BM162873.1 GI:17308554
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporidae; Plasmodium.
REFERENCE 1 (bases 1 to 621)
AUTHORS Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Valdivia, A.B.,
Fraser, C.M. and Carucci, D.J.
TITLE Plasmodium yoelii EST project at TIGR
JOURNAL Unpublished (2001)
COMMENT Contact: Jane Carlton
Parasite Genomics Group

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
<http://www.malaria.mr4.org/mr4pages/index.html>
Seq primer: ADF.

FEATURES
Location/Qualifiers
1..621
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/mol_type="mRNA"
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/sub_species="yoelii"
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/clone="PYCRX03"
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/lab_host="E. coli XL-1 Blue"
/clone_1db="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridZAP vector and plasmid DNA
isolated."

ORIGIN
Query Match 3.7%; Score 24; DB 12; Length 621;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 ATTAATGAATATCAAAAAGATATA 438
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49 ATTAATGAATATCAAAAAGATATA 72

Db

RESULT 3
CG185633/c 688 bp DNA linear GSS 21-AUG-2003
LOCUS PUC185633 688 bp DNA linear GSS 21-AUG-2003
DEFINITION PUC185633 2M.0.6.1.0 KB zea mays genomic clone ZMMB7a0552L16,
genomic survey sequence.
ACCESSION CG185633
VERSION CG185633.1 GI:34076694
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 688)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Reenick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.

TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUICP69TB
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source location/Qualifiers
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Cot selected genomic DNA library"

ORIGIN
Query Match 3.7%; Score 24; DB 29; Length 688;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 437 TATCTATTATTAATAATATTA 460
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Db 130 TATCTATTATTAATAATATTA 107

RESULT 4
B2728378/c 824 bp DNA linear GSS 03-MAR-2003
LOCUS OGCRC29TC ZM 0.7.1.5 KB Zea mays genomic clone ZMWERa0233E10,
DEFINITION genomic survey sequence.
ACCESSION B2728378
VERSION B2728378.1 GI:28701626
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 824)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Reenick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.

TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OGCRC29TC
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source location/Qualifiers
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/note="Vector: pBCSK-3; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 3.7%; Score 24; DB 28; Length 824;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 437 TATCTATTATTAATAATATTA 460
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Db 175 TATCTATTATTAATAATATTA 152

RESULT 5
CG296548/c 848 bp DNA linear GSS 25-AUG-2003
LOCUS OGBIC11TH ZM 0.7.1.5 KB Zea mays genomic clone ZMWERa0722A21,
DEFINITION genomic survey sequence.
ACCESSION CG296548
VERSION CG296548.1 GI:34210762
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 848)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Reenick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.

TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OGBIC11TV
Contact: Cathy Whitelaw
TIGR

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Tel: 301-838-5843
Fax: 301-838-0208

Email: white@sligr.org

Seq primer: TR

Class: sheared ends.

FEATURES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 265	18	6,9	237067	2	AC118339	AC118339	Rattus no	322	17	6,5	1838	5	AF22385553	AF2238554	Oncorhync
c 266	18	6,9	237712	9	AC012634	AC012634	Homo sapi	323	17	6,5	1838	5	AF22385853	AF2238585	Oncorhync
c 267	18	6,9	239623	2	AC121220	AC121220	Rattus no	324	17	6,5	1838	5	AF22386153	AF2238613	Oncorhync
c 268	18	6,9	240255	2	BX537326	BX537326	Danio rer	325	17	6,5	1838	5	AF22386453	AF2238643	Oncorhync
c 269	18	6,9	242384	2	AC105847	AC105847	Rattus no	326	17	6,5	1838	5	AF22386753	AF2238673	Oncorhync
c 270	18	6,9	242743	2	AC137367	AC137367	Rattus no	327	17	6,5	1838	5	AF22387053	AF2238703	Oncorhync
c 271	18	6,9	242907	2	AC106660	AC106660	Rattus no	328	17	6,5	1838	5	AF22387353	AF2238733	Oncorhync
c 272	18	6,9	243768	2	AC125725	AC125725	Rattus no	329	17	6,5	1838	5	AF22387653	AF2238763	Oncorhync
c 273	18	6,9	244974	2	AC111249	AC111249	Rattus no	330	17	6,5	1838	5	AF22387953	AF2238793	Oncorhync
c 274	18	6,9	250087	2	AC096831	AC096831	Rattus no	331	17	6,5	1838	5	AF22388253	AF2238823	Oncorhync
c 275	18	6,9	250337	2	AC098144	AC098144	Rattus no	332	17	6,5	1838	5	AF22388553	AF2238853	Oncorhync
c 276	18	6,9	251852	2	AC114625	AC114625	Mus muscu	333	17	6,5	1838	5	AF22388853	AF2238883	Oncorhync
c 277	18	6,9	252129	2	AC133975	AC133975	Rattus no	334	17	6,5	1879	6	BT000241	BT000240	Oncorhync
c 278	18	6,9	261938	2	AC105491	AC105491	Rattus no	335	17	6,5	1947	6	AR321206	AR321205	Oncorhync
c 279	18	6,9	263855	2	AC127797	AC127797	Rattus no	336	17	6,5	2002	8	AY099582	AY099581	Oncorhync
c 280	18	6,9	265977	2	AC134623	AC134623	Mus muscu	337	17	6,5	2109	8	BT003163	BT003162	Oncorhync
c 281	18	6,9	266574	2	AC087129	AC087129	Mus muscu	338	17	6,5	2159	9	HS026396	HS026395	Oncorhync
c 282	18	6,9	267326	2	AC110972	AC110972	Rattus no	339	17	6,5	2247	3	DM066460	DM066459	Oncorhync
c 283	18	6,9	269296	2	AC107602	AC107602	Rattus no	340	17	6,5	2318	5	ONHP501	ONHP500	Oncorhync
c 284	18	6,9	271788	2	AC110973	AC110973	Rattus no	341	17	6,5	2534	1	ECRCGB	ECRCGB	Oncorhync
c 285	18	6,9	276372	2	AC125569	AC125569	Rattus no	342	17	6,5	2551	8	SCPGM1A	SCPGM1A	Oncorhync
c 286	18	6,9	278227	2	AC128099	AC128099	Rattus no	343	17	6,5	2552	2	AC020498	AC020497	Oncorhync
c 287	18	6,9	279666	2	AC130931	AC130931	Rattus no	344	17	6,5	2625	8	AK070975	AK070974	Oncorhync
c 288	18	6,9	280394	2	AE003544	AE003544	Drosophill	345	17	6,5	2671	5	D1063653	D1063652	Oncorhync
c 289	18	6,9	333192	2	AC113779	AC113779	Rattus no	346	17	6,5	2760	9	HUMLEP0D	HUMLEP0D	Oncorhync
c 290	18	6,9	340000	9	AP001718	AP001718	Homo sapi	347	17	6,5	2875	8	AY383719	AY383718	Oncorhync
c 291	18	6,9	349505	2	AC130443	AC130443	Rattus no	348	17	6,5	3024	10	BC057064	BC057063	Oncorhync
c 292	18	6,9	349505	2	AC130443	AC130443	Rattus no	349	17	6,5	3452	3	AY128432	AY128431	Oncorhync
c 293	17	6,5	232	6	AR251699	AR251699	Sequence	350	17	6,5	3476	3	BT009935	BT009934	Oncorhync
c 294	17	6,5	401	6	AX321179	AX321179	Sequence	351	17	6,5	3577	3	DM005A	DM005A	Oncorhync
c 295	17	6,5	441	6	AX570166	AX570166	Sequence	352	17	6,5	3618	9	HUMTRP	HUMTRP	Oncorhync
c 296	17	6,5	607	11	BV040243	BV040243	Sequence	353	17	6,5	3935	8	SCYK127W	SCYK127W	Oncorhync
c 297	17	6,5	647	8	AJ600965	AJ600965	Arbidiops	354	17	6,5	4077	10	BC064438	BC064437	Oncorhync
c 298	17	6,5	785	6	BD019595	BD019595	Novel gen	355	17	6,5	4513	10	BC027791	BC027790	Oncorhync
c 299	17	6,5	785	6	BD099533	BD099533	Novel gen	356	17	6,5	4734	9	HS0800826	HS0800825	Oncorhync
c 300	17	6,5	785	6	BD186809	BD186809	Nucleic a	357	17	6,5	5355	6	E30079	E30079	Oncorhync
c 301	17	6,5	786	11	BV038169	BV038169	Novel gen	358	17	6,5	5355	6	E30080	E30080	Oncorhync
c 302	17	6,5	1021	8	GN251539	AJ251539	Gnetum gn	359	17	6,5	5355	9	AB011422	AB011421	Oncorhync
c 303	17	6,5	1146	10	MEF0DA	X12801	Murine mRNA	360	17	6,5	5777	8	ATH133743	ATH133742	Oncorhync
c 304	17	6,5	1284	5	XERAND	Z95080	X. laevis mr	361	17	6,5	5830	9	HS0807900	HS0807899	Oncorhync
c 305	17	6,5	1593	8	AK070418	AK070418	Oryza sat	362	17	6,5	6497	8	AF159061	AF159060	Oncorhync
c 306	17	6,5	1597	5	BC049424	BC049424	Danio rer	363	17	6,5	6514	9	AF148808	AF148807	Oncorhync
c 307	17	6,5	1597	5	BC053150	BC053150	Danio rer	364	17	6,5	7172	6	AR218888	AR218887	Oncorhync
c 308	17	6,5	1781	9	HS0805147	AL633859	Homo sapi	365	17	6,5	7172	6	BD003800	BD003799	Oncorhync
c 309	17	6,5	1837	5	AF22388253	AF2238824	Oncorhync	366	17	6,5	7672	6	AR274887	AR274886	Oncorhync
c 310	17	6,5	1838	5	AF22381953	AF223824	Oncorhync	367	17	6,5	7672	6	AK780070	AK780069	Oncorhync
c 311	17	6,5	1838	5	AF22382253	AF223827	Oncorhync	368	17	6,5	7787	6	AX334524	AX334523	Oncorhync
c 312	17	6,5	1838	5	AF22382553	AF223830	Oncorhync	369	17	6,5	7827	9	HUMASPX	HUMASPX	Oncorhync
c 313	17	6,5	1838	5	AF22382853	AF223833	Oncorhync	370	17	6,5	10029	1	AE005451	AE005450	Oncorhync
c 314	17	6,5	1838	5	AF22383153	AF223836	Oncorhync	371	17	6,5	10189	1	AE005549	AE005548	Oncorhync
c 315	17	6,5	1838	5	AF22383453	AF223839	Oncorhync	372	17	6,5	10189	1	AE015336	AE015335	Oncorhync
c 316	17	6,5	1838	5	AF22383753	AF223842	Oncorhync	373	17	6,5	10189	1	AE015336	AE015335	Oncorhync
c 317	17	6,5	1838	5	AF22384053	AF223845	Oncorhync	374	17	6,5	10189	1	AE015336	AE015335	Oncorhync
c 318	17	6,5	1838	5	AF22384353	AF223848	Oncorhync	375	17	6,5	10382	1	AE008517	AE008516	Oncorhync

c 376	17	6.5	10846	1	AE013594	AE013594 Methanosa	433	17	6.5	83511	8	AB013389	AB013389 Arabidops
c 377	17	6.5	11857	2	AC018239	AC018239 Drosophill	c 434	17	6.5	83537	9	AL138735	AL138735 Human DNA
c 378	17	6.5	14295	1	AE000400	AE000400 Escherich	c 435	17	6.5	84551	3	AC004295	AC004295 Drosophill
c 379	17	6.5	14764	10	AL974311	AL974311 Mouse DNA	c 436	17	6.5	85785	8	ATP21P8	ATP21P8 Arabidops
c 380	17	6.5	16697	9	AL591687	AL591687 Human DNA	c 437	17	6.5	90463	8	AP003810	AP003810 Oryza sat
c 381	17	6.5	24139	10	AF463765	AF463765 Mus muscu	c 438	17	6.5	90875	5	AL672192	AL672192 Zebrafish
c 382	17	6.5	24667	9	AF001295	AF001295 Homo sapi	c 439	17	6.5	91025	9	AL3559270	AL3559270 Human DNA
c 383	17	6.5	25464	6	AP1686	AP1686 Sequence 4	c 440	17	6.5	91059	9	AP003463	AP003463 Homo sapi
c 384	17	6.5	25464	6	AR307527	AR307527 Sequence	c 441	17	6.5	93217	2	AC023171	AC023171 Homo sapi
c 385	17	6.5	25464	6	BD023455	BD023455 Nucleotid	c 442	17	6.5	93586	9	AL590487	AL590487 Human DNA
c 386	17	6.5	26514	2	AC005649	AC005649 Drosophill	c 443	17	6.5	94802	2	SPNEU1913	SPNEU1913 Streptoco
c 387	17	6.5	27503	9	AL160404	AL160404 Human DNA	c 444	17	6.5	94924	2	AL355997	AL355997 Human DNA
c 388	17	6.5	28716	10	AL928795	AL928795 Mouse DNA	c 445	17	6.5	98878	2	AC087108	AC087108 Homo sapi
c 389	17	6.5	30985	8	SPAC9G1	Z98765 S.pombe chr	c 446	17	6.5	101029	9	AC026934	AC026934 Homo sapi
c 390	17	6.5	31151	2	AC107201	Continuation (9 of	c 447	17	6.5	101333	8	AP004030	AP004030 Oryza sat
c 391	17	6.5	31957	3	AC004267	AC004267 Drosophill	c 448	17	6.5	101882	9	AC021089	AC021089 Homo sapi
c 392	17	6.5	32479	2	AC090240	AC090240 Homo sapi	c 449	17	6.5	101923	10	AC138172	AC138172 Mus muscu
c 393	17	6.5	38692	3	AC116919	AC116919 Dictyoste	c 450	17	6.5	102282	9	AL158033	AL158033 Human DNA
c 394	17	6.5	39013	1	AF088896	AF088896 Zygomonas	c 451	17	6.5	102965	2	AC146727	AC146727 Ocotlemar
c 395	17	6.5	39938	9	AL590456	AL590456 Human DNA	c 452	17	6.5	103390	9	AL358533	AL358533 Human DNA
c 396	17	6.5	40699	8	SPBC119	AL022117 S.pombe c	c 453	17	6.5	103479	9	AC140059	AC140059 Homo sapi
c 397	17	6.5	40753	3	BFY18367	Y18367 Branchiosto	c 454	17	6.5	103523	9	AL590408	AL590408 Human DNA
c 398	17	6.5	45014	2	AC147003	AC147003 Homo sapi	c 455	17	6.5	105070	8	AP006352	AP006352 Lotus cor
c 399	17	6.5	45472	3	CEY59A8A	AL132895 Caenorhab	c 456	17	6.5	105600	8	AP005173	AP005173 Oryza sat
c 400	17	6.5	51648	2	AC015434	AC015434 Drosophill	c 457	17	6.5	105695	2	BX571758	BX571758 Dario rer
c 401	17	6.5	51860	10	AL080109	AL080109 Mouse DNA	c 458	17	6.5	105961	2	AC119411	AC119411 Medicago
c 402	17	6.5	52417	9	AC114777	AC114777 Homo sapi	c 459	17	6.5	106975	8	OSDN00045	OSDN00045 Oryza sat
c 403	17	6.5	53411	2	AC087287	AC087287 Homo sapi	c 460	17	6.5	107025	2	AL139235	AL139235 Continuation (4 of
c 404	17	6.5	55543	9	AL139152	AL139152 Human DNA	c 461	17	6.5	109685	9	AC024578	AC024578 Homo sapi
c 405	17	6.5	55687	9	AC079464	AC079464 Homo sapi	c 462	17	6.5	110000	1	ECOM67_1	ECOM67_1 Continuation (2 of
c 406	17	6.5	57198	2	AL590066	Continuation (4 of	c 463	17	6.5	110000	2	AC101676	AC101676 Continuation (3 of
c 407	17	6.5	58190	9	HS498124	AL031057 Human DNA	c 464	17	6.5	110000	2	AC107201	AC107201 Continuation (8 of
c 408	17	6.5	58449	10	AL929218	AL929218 Mouse DNA	c 465	17	6.5	110000	2	AC112133	AC112133 Homo sapi
c 409	17	6.5	59219	2	AC090385	AC090385 Homo sapi	c 466	17	6.5	110000	2	AC113868	AC113868 Continuation (3 of
c 410	17	6.5	59303	8	AP004555	AP004555 Lotus cor	c 467	17	6.5	110000	2	AC116279	AC116279 Rattus no
c 411	17	6.5	61150	2	AC100284	AC100284 Mus muscu	c 468	17	6.5	110000	2	AC118411	AC118411 Rattus no
c 412	17	6.5	61725	2	AC100105	AC100105 Mus muscu	c 469	17	6.5	110000	2	AC120762	AC120762 Continuation (3 of
c 413	17	6.5	62219	2	AC120844	AC120844 Mus muscu	c 470	17	6.5	110000	2	AC123241	AC123241 Continuation (3 of
c 414	17	6.5	63268	2	AC103683	AC103683 Homo sapi	c 471	17	6.5	110000	2	AC132794	AC132794 Continuation (2 of
c 415	17	6.5	63268	2	AC103683	AC103683 Homo sapi	c 472	17	6.5	110000	2	AC141403	AC141403 Continuation (3 of
c 416	17	6.5	64139	9	AC069064	AC069064 Homo sapi	c 473	17	6.5	110000	2	AL139235	AL139235 Continuation (2 of
c 417	17	6.5	64208	9	AL929000	AL929000 Human DNA	c 474	17	6.5	110000	2	BX294176	BX294176 Continuation (3 of
c 418	17	6.5	64786	2	AC017805	AC017805 Drosophill	c 475	17	6.5	110000	2	PFPA113_01	PFPA113_01 Continuation (3 of
c 419	17	6.5	64849	2	AC113037	AC113037 Mus muscu	c 476	17	6.5	110000	2	AL359675	AL359675 Continuation (2 of
c 420	17	6.5	65014	2	AC100176	AC100176 Mus muscu	c 477	17	6.5	110991	9	AC091983	AC091983 Human DNA
c 421	17	6.5	66137	2	AC101526	AC101526 Mus muscu	c 478	17	6.5	114026	9	AL365201	AL365201 Human DNA
c 422	17	6.5	66310	2	AC135728	AC135728 Homo sapi	c 479	17	6.5	114626	4	AC138157	AC138157 Streptoco
c 423	17	6.5	69314	9	AY129465	Continuation (5 of	c 480	17	6.5	115040	8	AC124954	AC124954 Medicago
c 424	17	6.5	71380	9	AC092605	AC092605 Homo sapi	c 481	17	6.5	115424	2	AC146806	AC146806 Medicago
c 425	17	6.5	72591	2	AC080137	AC080137 Homo sapi	c 482	17	6.5	117217	9	AP002076	AP002076 Homo sapi
c 426	17	6.5	73184	2	AC090864	AC090864 Homo sapi	c 483	17	6.5	117217	9	HS117P19	HS117P19 Human DNA
c 427	17	6.5	78054	3	AC004296	AC004296 Drosophill	c 484	17	6.5	118755	9	AC090152	AC090152 Homo sapi
c 428	17	6.5	78643	3	AC004352	AC004352 Drosophill	c 485	17	6.5	118869	9	AC004903	AC004903 Homo sapi
c 429	17	6.5	81147	9	AL606504	AL606504 Human DNA	c 486	17	6.5	119491	9	AC098860	AC098860 Homo sapi
c 430	17	6.5	81476	10	BX004788	BX004788 Mouse DNA	c 487	17	6.5	119875	9	AC108051	AC108051 Homo sapi
c 431	17	6.5	82064	2	AC006937	AC006937 Drosophill	c 488	17	6.5	120562	8	AT268139	AT268139 Oryza sat
c 432	17	6.5	83490	8	AP004039	AP004039 Oryza sat	c 489	17	6.5	120562	8	AT268139	AT268139 Oryza sat

490	17	6.5	120625	2	AC017563	AC017563 Drosophila
491	17	6.5	121141	10	AC125314	AC125314 Mus muscu
492	17	6.5	122681	1	AC096062	AC096062 Homo sapi
493	17	6.5	123386	8	F12F1	AC002131 Arabidops
494	17	6.5	124214	9	AL807246	AL807246 Human DNA
495	17	6.5	125439	9	AC138990	AC138990 Homo sapi
496	17	6.5	125527	9	AL353133	AL353133 Human DNA
497	17	6.5	125760	2	AC080122	AC080122 Homo sapi
498	17	6.5	125785	9	AC107393	AC107393 Homo sapi
499	17	6.5	125973	2	AC010353	AC010353 Homo sapi
500	17	6.5	127178	9	AC005160	AC005160 Homo sapi
501	17	6.5	127472	2	AC124962	AC124962 Medicago
502	17	6.5	128016	2	AC138131	AC138131 Medicago
503	17	6.5	128218	2	AC121096	AC121096 Mus muscu
504	17	6.5	128751	5	BX649586	BX649586 Zebrafish
505	17	6.5	128965	9	AL357562	AL357562 Human DNA
506	17	6.5	129083	2	AC096853	AC096853 Sus scrofa
507	17	6.5	129984	9	AC115620	AC115620 Homo sapi
508	17	6.5	130361	10	AL929546	AL929546 Mouse DNA
509	17	6.5	130586	2	AC073238	AC073238 Homo sapi
510	17	6.5	130632	2	AC004547	AC004547 Homo sapi
511	17	6.5	131704	2	AP004313	AP004313 Oryza sat
512	17	6.5	132200	2	AL161619	AL161619 Homo sapi
513	17	6.5	132782	8	AC120983	AC120983 Oryza sat
514	17	6.5	132927	8	AC079890	AC079890 Oryza sat
515	17	6.5	133157	9	AC109351	AC109351 Homo sapi
516	17	6.5	133330	10	AL928871	AL928871 Mouse DNA
517	17	6.5	133513	9	BS000023	BS000023 Pan trogl
518	17	6.5	136164	3	AC099006	AC099006 Drosophila
519	17	6.5	136551	9	AC123786	AC123786 Homo sapi
520	17	6.5	136901	9	AC073626	AC073626 Homo sapi
521	17	6.5	136906	2	RN86120	AL603805 Nectus no
522	17	6.5	137289	9	AC022828	AC022828 Homo sapi
523	17	6.5	137441	5	AL928712	AL928712 Zebrafish
524	17	6.5	137445	2	AP004780	AP004780 Oryza sat
525	17	6.5	137985	2	AP005634	AP005634 Oryza sat
526	17	6.5	138419	9	AL137793	AL137793 Human DNA
527	17	6.5	138769	2	BX571896	BX571896 Danio rer
528	17	6.5	139033	9	HSJ080804	AL409364 Homo sapi
529	17	6.5	140606	2	AL353761	AL353761 Homo sapi
530	17	6.5	140680	2	BX510917	BX510917 Danio rer
531	17	6.5	141889	2	AC032006	AC032006 Homo sapi
532	17	6.5	142021	10	AL645843	AL645843 Mouse DNA
533	17	6.5	142123	2	AC068890	AC068890 Homo sapi
534	17	6.5	142353	2	AC073286	AC073286 Homo sapi
535	17	6.5	142911	2	BX855398	BX855398 Danio rer
536	17	6.5	142959	2	AC025453	AC025453 Homo sapi
537	17	6.5	143146	9	AC079855	AC079855 Homo sapi
538	17	6.5	143687	9	AC016572	AC016572 Homo sapi
539	17	6.5	144062	5	AL954190	AL954190 Zebrafish
540	17	6.5	144631	9	AC069027	AC069027 Homo sapi
541	17	6.5	144649	2	AC145841	AC145841 Medicago
542	17	6.5	144879	2	AC138597	AC138597 Mus muscu
543	17	6.5	145085	2	AC090261	AC090261 Homo sapi
544	17	6.5	145173	9	AC005599	AC005599 Homo sapi
545	17	6.5	145629	2	BX322794	BX322794 Danio rer
546	17	6.5	145829	2	BX571953	BX571953 Danio rer
547	17	6.5	145913	2	AP005821	AP005821 Oryza sat
548	17	6.5	145947	9	AL353588	AL353588 Human DNA
549	17	6.5	146170	2	AC079224	AC079224 Homo sapi
550	17	6.5	146275	2	AC080119	AC080119 Homo sapi
551	17	6.5	146396	10	AL929449	AL929449 Mouse DNA
552	17	6.5	146468	2	AC181626	AC181626 Rattus no
553	17	6.5	146690	2	AC102254	AC102254 Mus muscu
554	17	6.5	146810	9	AC084706	AC084706 Homo sapi
555	17	6.5	146952	9	AC068522	AC068522 Homo sapi
556	17	6.5	147008	2	AC138980	AC138980 Homo sapi
557	17	6.5	147177	2	AC138981	AC138981 Homo sapi
558	17	6.5	148003	2	BX373720	BX373720 Danio rer
559	17	6.5	148085	2	AC123364	AC123364 Rattus no
560	17	6.5	149143	2	AC092974	AC092974 Homo sapi
561	17	6.5	149428	2	AC010264	AC010264 Homo sapi
562	17	6.5	149559	9	AL139327	AL139327 Human DNA
563	17	6.5	149901	2	AC022243	AC022243 Homo sapi
564	17	6.5	150026	2	AL188986	AL188986 Homo sapi
565	17	6.5	150096	2	AC117562	AC117562 Mus muscu
566	17	6.5	150350	9	CNS01DW	AL138533 Human chr
567	17	6.5	150355	9	HSJ364H0	AL079603 Human DNA
568	17	6.5	150399	9	AC093680	AC093680 Homo sapi
569	17	6.5	150400	10	AC122911	AC122911 Mus muscu
570	17	6.5	150887	2	AC018580	AC018580 Homo sapi
571	17	6.5	151203	8	CNS054W	BX55875 Oryza sat
572	17	6.5	151319	9	AC108036	AC108036 Homo sapi
573	17	6.5	151540	2	AL772252	AL772252 Homo sapi
574	17	6.5	151696	2	AP001768	AP001768 Homo sapi
575	17	6.5	151761	9	HSJ493D19	AL096868 Human DNA
576	17	6.5	151822	9	AC004478	AC004478 Homo sapi
577	17	6.5	152081	9	AC007381	AC007381 Homo sapi
578	17	6.5	152464	2	AC023473	AC023473 Homo sapi
579	17	6.5	152454	2	AC067909	AC067909 Homo sapi
580	17	6.5	153064	8	CNS08CAL	AL831808 Oryza sat
581	17	6.5	153155	2	AC060783	AC060783 Homo sapi
582	17	6.5	153319	2	AC136027	AC136027 Mus muscu
583	17	6.5	153402	9	HS247BZ	AL773563 Homo sapi
584	17	6.5	153533	2	AC124338	AC124338 Mus muscu
585	17	6.5	153716	9	AL590631	AL590631 Human DNA
586	17	6.5	154016	2	AC091311	AC091311 Mus muscu
587	17	6.5	154323	2	AC025831	AC025831 Homo sapi
588	17	6.5	154417	2	AC102530	AC102530 Mus muscu
589	17	6.5	154455	2	AC021844	AC021844 Homo sapi
590	17	6.5	154604	5	AL954739	AL954739 Zebrafish
591	17	6.5	154753	2	AC020605	AC020605 Homo sapi
592	17	6.5	154758	9	AC112491	AC112491 Human chr
593	17	6.5	155326	9	CNS07EF2	AL512311 Human chr
594	17	6.5	155394	2	AC092328	AC092328 Homo sapi
595	17	6.5	156142	3	AC091228	AC091228 Homo sapi
596	17	6.5	156190	2	AC097651	AC097651 Homo sapi
597	17	6.5	156332	10	AC116581	AC116581 Mus muscu
598	17	6.5	156392	9	AC026341	AC026341 Homo sapi
599	17	6.5	157067	2	AC137265	AC137265 Rattus no
600	17	6.5	157393	2	AC036212	AC036212 Homo sapi
601	17	6.5	157591	2	BX323068	BX323068 Danio rer
602	17	6.5	157747	2	AC067915	AC067915 Homo sapi
603	17	6.5	157816	9	AC093666	AC093666 Homo sapi

604	17	6.5 157949	9	AL355578	AL355578 Human DNA	c 661	17	6.5 168197	9	AC023307	AC023307 Homo sapi
605	17	6.5 158600	2	BX296541	BX296541 Dantio rer	c 662	17	6.5 168306	3	AC008135	AC008135 Drosophila
606	17	6.5 158684	2	AC079493	AC079493 Mus muscu	c 663	17	6.5 168431	2	BX470138	BX470138 Dantio rer
607	17	6.5 158830	10	AC131740	AC131740 Mus muscu	c 664	17	6.5 168843	2	AC091711	AC091711 Rattus no
608	17	6.5 159013	2	BX323995	BX323995 Dantio rer	c 665	17	6.5 168966	2	AC015785	AC015785 Homo sapi
609	17	6.5 159024	2	AC025495	AC025495 Homo sapi	c 666	17	6.5 169083	2	AL155346	AL155346 Homo sapi
610	17	6.5 159188	2	AC037432	AC037432 Homo sapi	c 667	17	6.5 169479	2	BX890540	BX890540 Dantio rer
611	17	6.5 159242	2	AC078800	AC078800 Homo sapi	c 668	17	6.5 169557	5	AL928999	AL928999 Zebrafish
612	17	6.5 159300	9	HS279E22	AL662879 Homo sapi	c 669	17	6.5 169570	5	AL928999	AL928999 Zebrafish
613	17	6.5 159331	9	AL589741	AL589741 Human DNA	c 670	17	6.5 169628	5	BX322567	BX322567 Zebrafish
614	17	6.5 160002	5	BX000446	BX000446 Zebrafish	c 671	17	6.5 170001	9	HS452521	AL021917 Human DNA
615	17	6.5 160069	2	AC064867	AC064867 Homo sapi	c 672	17	6.5 170311	9	AC021701	AC021701 Homo sapi
616	17	6.5 160197	2	AC115700	AC115700 Mus muscu	c 673	17	6.5 170625	2	AC144620	AC144620 Mus muscu
617	17	6.5 160302	9	AC010685	AC010685 Homo sapi	c 674	17	6.5 170682	2	AC021245	AC021245 Homo sapi
618	17	6.5 160624	2	AC144418	AC144418 Rattus no	c 675	17	6.5 170817	9	AL513166	AL513166 Human DNA
619	17	6.5 161054	2	AC123744	AC123744 Mus muscu	c 676	17	6.5 170849	2	AC109803	AC109803 Homo sapi
620	17	6.5 161364	2	AC068637	AC068637 Homo sapi	c 677	17	6.5 170923	2	AC110042	AC110042 Mus muscu
621	17	6.5 161638	9	AC107934	AC107934 Homo sapi	c 678	17	6.5 171206	2	AC026573	AC026573 Homo sapi
622	17	6.5 161672	2	AC136667	AC136667 Rattus no	c 679	17	6.5 171375	3	AC007082	AC007082 Drosophila
623	17	6.5 162046	2	AC127375	AC127375 Mus muscu	c 680	17	6.5 171686	9	AC142284	AC142284 Pan trogl
624	17	6.5 162075	9	HS12703	AL021026 Human DNA	c 681	17	6.5 171721	9	AC022821	AC022821 Homo sapi
625	17	6.5 162151	9	AL138753	AL138753 Human DNA	c 682	17	6.5 171742	2	BX897662	BX897662 Dantio rer
626	17	6.5 162411	2	AC147061	AC147061 Pan trogl	c 683	17	6.5 171887	2	AL356355	AL356355 Homo sapi
627	17	6.5 162880	2	AC120363	AC120363 Mus muscu	c 684	17	6.5 171930	2	AC118687	AC118687 Mus muscu
628	17	6.5 162922	2	AC011281	AC011281 Homo sapi	c 685	17	6.5 172018	2	AC107672	AC107672 Mus muscu
629	17	6.5 162995	10	AL663032	AL663032 Mouse DNA	c 686	17	6.5 172475	9	AL358972	AL358972 Human DNA
630	17	6.5 163066	2	AC116506	AC116506 Mus muscu	c 687	17	6.5 172606	9	AL358953	AL358953 Homo sapi
631	17	6.5 163110	2	AC068705	AC068705 Homo sapi	c 688	17	6.5 173031	9	AL359853	AL359853 Human DNA
632	17	6.5 163231	9	AL162575	AL162575 Human DNA	c 689	17	6.5 173045	2	AC120413	AC120413 Mus muscu
633	17	6.5 163357	2	AC023276	AC023276 Homo sapi	c 690	17	6.5 173177	2	AC102661	AC102661 Mus muscu
634	17	6.5 163404	2	AC118883	AC118883 Rattus no	c 691	17	6.5 173415	9	CNS01DVS	AC102661 Mus muscu
635	17	6.5 163443	5	AL1773542	AL1773542 Zebrafish	c 692	17	6.5 173564	5	BX470230	BX470230 Zebrafish
636	17	6.5 163706	2	AL354927	AL354927 Homo sapi	c 693	17	6.5 173756	2	AC134948	AC134948 Rattus no
637	17	6.5 163712	9	AC004065	AC004065 Homo sapi	c 694	17	6.5 173911	10	AL669819	AL669819 Human DNA
638	17	6.5 164007	2	AC069218	AC069218 Homo sapi	c 695	17	6.5 173966	2	AC138365	AC138365 Mus muscu
639	17	6.5 164118	2	AC021384	AC021384 Homo sapi	c 696	17	6.5 173987	10	AL670250	AL670250 Mouse DNA
640	17	6.5 164278	2	AC073126	AC073126 Homo sapi	c 697	17	6.5 174151	10	AL672050	AL672050 Mouse DNA
641	17	6.5 164799	2	BX511121	BX511121 Dantio rer	c 698	17	6.5 174151	10	AL672050	AL672050 Mouse DNA
642	17	6.5 165011	9	AL445255	AL445255 Human DNA	c 699	17	6.5 174171	2	AC134519	AC134519 Homo sapi
643	17	6.5 165089	9	AC021646	AC021646 Homo sapi	c 700	17	6.5 174286	2	AC116795	AC116795 Mus muscu
644	17	6.5 165768	2	AC023517	AC023517 Homo sapi	c 701	17	6.5 174301	5	AL845287	AL845287 Zebrafish
645	17	6.5 165798	2	AC117794	AC117794 Mus muscu	c 702	17	6.5 174347	10	AL928956	AL928956 Mouse DNA
646	17	6.5 166007	9	CNS01DRC	AL117186 Human chr	c 703	17	6.5 174473	5	AL928514	AL928514 Zebrafish
647	17	6.5 166071	9	AC022336	AC022336 Homo sapi	c 704	17	6.5 174530	9	AC009166	AC009166 Homo sapi
648	17	6.5 166168	2	AC115193	AC115193 Rattus no	c 705	17	6.5 174638	10	AL670290	AL670290 Mouse DNA
649	17	6.5 166174	2	AC009633	AC009633 Homo sapi	c 706	17	6.5 174700	2	AC025344	AC025344 Homo sapi
650	17	6.5 166231	9	AL773537	AL773537 Human DNA	c 707	17	6.5 174741	2	AC073119	AC073119 Homo sapi
651	17	6.5 166525	9	AC022413	AC022413 Homo sapi	c 708	17	6.5 174775	5	BX828491	BX828491 Zebrafish
652	17	6.5 166531	2	BX890591	BX890591 Dantio rer	c 709	17	6.5 175380	2	AL512411	AL512411 Homo sapi
653	17	6.5 166651	4	AC087160	AC087160 Sus scrofa	c 710	17	6.5 175384	9	CNS07EFV	AL512411 Homo sapi
654	17	6.5 166716	2	AC108482	AC108482 Homo sapi	c 711	17	6.5 175666	9	AL356481	AL356481 Human chr
655	17	6.5 167162	2	AC139872	AC139872 Rattus no	c 712	17	6.5 176097	9	AL591438	AL591438 Human DNA
656	17	6.5 167214	2	AC096202	AC096202 Rattus no	c 713	17	6.5 176233	10	AL732417	AL732417 Mouse DNA
657	17	6.5 167853	2	AP001798	AP001798 Homo sapi	c 714	17	6.5 176243	2	AC145095	AC145095 Homo sapi
658	17	6.5 167974	9	AL591073	AL591073 Human DNA	c 715	17	6.5 176248	9	AC007498	AC007498 Homo sapi
659	17	6.5 168043	2	AC011935	AC011935 Homo sapi	c 716	17	6.5 176267	9	AC113420	AC113420 Homo sapi
660	17	6.5 168108	9	AL445687	AL445687 Human DNA	c 717	17	6.5 176267	9	AC113420	AC113420 Homo sapi

c 718	17	6.5 176350	2	AC092513	AC092513 Papio anu	c 775	17	6.5 184861	2	BX296527	BX296527 Dantio rer
c 719	17	6.5 176863	2	AL358353	AL358353 Homo sapi	c 776	17	6.5 185029	9	AC090707	AC090707 Homo sapi
c 720	17	6.5 177083	3	AC008285	AC008285 Drosophi1	c 777	17	6.5 185116	9	AC005823	AC005823 Homo sapi
c 721	17	6.5 177112	9	AC002452	AC002452 Homo sapi	c 778	17	6.5 185123	2	AC053524	AC053524 Homo sapi
c 722	17	6.5 177145	2	AC113156	AC113156 Homo sapi	c 779	17	6.5 185135	5	BX005248	BX005248 Zebrafish
c 723	17	6.5 177202	2	AC118703	AC118703 Mus muscu	c 780	17	6.5 185320	8	AP006101	AP006101 Lotus cor
c 724	17	6.5 177528	2	AC093444	AC093444 Pen trogl	c 781	17	6.5 185333	2	AC113288	AC113288 Mus muscu
c 725	17	6.5 177599	2	AC097630	AC097630 Sus scrof	c 782	17	6.5 185623	2	AC137058	AC137058 Homo sapi
c 726	17	6.5 177797	2	AC140039	AC140039 Mus muscu	c 783	17	6.5 185652	9	AC007312	AC007312 Homo sapi
c 727	17	6.5 178212	2	AC013326	AC013326 Homo sapi	c 784	17	6.5 185680	10	AC131751	AC131751 Mus muscu
c 728	17	6.5 178311	9	AC104795	AC104795 Homo sapi	c 785	17	6.5 185693	2	AC128182	AC128182 Rattus no
c 729	17	6.5 178742	2	AC134807	AC134807 Rattus no	c 786	17	6.5 185791	9	AC098861	AC098861 Homo sapi
c 730	17	6.5 179269	9	AC093627	AC093627 Homo sapi	c 787	17	6.5 186044	2	AC087674	AC087674 Homo sapi
c 731	17	6.5 179270	9	AC104580	AC104580 Homo sapi	c 788	17	6.5 186239	9	AC123982	AC123982 Pen trogl
c 732	17	6.5 179437	5	AL928892	AL928892 Zebrafish	c 789	17	6.5 186285	2	AC140098	AC140098 Sus scrof
c 733	17	6.5 179767	2	AC114584	AC114584 Mus muscu	c 790	17	6.5 186369	9	AC044814	AC044814 Homo sapi
c 734	17	6.5 180000	2	AC004578	AC004578 Homo sapi	c 791	17	6.5 186687	9	AC134943	AC134943 Homo sapi
c 735	17	6.5 180104	9	DJ326N18	AF123462 Homo sapi	c 792	17	6.5 186765	2	AC016992	AC016992 Homo sapi
c 736	17	6.5 180166	2	AC011898	AC011898 Homo sapi	c 793	17	6.5 186780	9	AC005740	AC005740 Homo sapi
c 737	17	6.5 180179	2	AC018881	AC018881 Homo sapi	c 794	17	6.5 186798	10	AC140980	AC140980 Mus muscu
c 738	17	6.5 180273	2	AP002894	AP002894 Homo sapi	c 795	17	6.5 187081	2	AC110735	AC110735 Mus muscu
c 739	17	6.5 180359	2	AC022064	AC022064 Homo sapi	c 796	17	6.5 187136	9	AC114316	AC114316 Homo sapi
c 740	17	6.5 180534	2	CNS08CB7	AL845345 Oryza sat	c 797	17	6.5 187349	2	AC137270	AC137270 Mus muscu
c 741	17	6.5 180766	9	AC090691	AC090691 Homo sapi	c 798	17	6.5 187615	2	AC020724	AC020724 Homo sapi
c 742	17	6.5 180947	2	AC128079	AC128079 Rattus no	c 799	17	6.5 187833	9	AL513303	AL513303 Human DNA
c 743	17	6.5 180995	9	AC117500	AC117500 Homo sapi	c 800	17	6.5 187914	2	AC141124	AC141124 Rattus no
c 744	17	6.5 181033	10	AL731663	AL731663 Mouse DNA	c 801	17	6.5 187936	9	AC080003	AC080003 Homo sapi
c 745	17	6.5 181036	9	AC087683	AC087683 Homo sapi	c 802	17	6.5 188047	2	AC022995	AC022995 Homo sapi
c 746	17	6.5 181124	2	AP002390	AP002390 Homo sapi	c 803	17	6.5 188211	9	AL358073	AL358073 Human DNA
c 747	17	6.5 181174	2	AC112626	AC112626 Rattus no	c 804	17	6.5 188248	2	AC131928	AC131928 Homo sapi
c 748	17	6.5 181294	2	AC024172	AC024172 Homo sapi	c 805	17	6.5 188337	5	BX005021	BX005021 Zebrafish
c 749	17	6.5 181384	10	AL732508	AL732508 Mouse DNA	c 806	17	6.5 188481	9	AL138836	AL138836 Human DNA
c 750	17	6.5 181407	2	AC113433	AC113433 Rattus no	c 807	17	6.5 188486	2	AP001796	AP001796 Homo sapi
c 751	17	6.5 181567	9	AL845426	AL845426 Mouse DNA	c 808	17	6.5 188532	2	AC145036	AC145036 Homo sapi
c 752	17	6.5 181910	10	AL672179	AL672179 Mouse DNA	c 809	17	6.5 188717	2	AC110117	AC110117 Rattus no
c 753	17	6.5 182019	9	AC007077	AC007077 Homo sapi	c 810	17	6.5 188775	2	AC026537	AC026537 Homo sapi
c 754	17	6.5 182087	2	AC054790	AC054790 Homo sapi	c 811	17	6.5 188970	2	BX247878	BX247878 Dantio rer
c 755	17	6.5 182556	9	AC016879	AC016879 Homo sapi	c 812	17	6.5 189054	2	AC131458	AC131458 Rattus no
c 756	17	6.5 182643	2	AP002794	AP002794 Homo sapi	c 813	17	6.5 189315	10	AL606508	AL606508 Mouse DNA
c 757	17	6.5 182700	2	AC145747	AC145747 Mus muscu	c 814	17	6.5 189720	2	BX470241	BX470241 Dantio rer
c 758	17	6.5 182725	2	AC021206	AC021206 Homo sapi	c 815	17	6.5 189748	2	AC140866	AC140866 Homo sapi
c 759	17	6.5 182752	2	BX510936	BX510936 Dantio rer	c 816	17	6.5 189854	9	AC093686	AC093686 Homo sapi
c 760	17	6.5 182871	3	AC117176	AC117176 Drosophi1	c 817	17	6.5 189940	2	AC051647	AC051647 Homo sapi
c 761	17	6.5 182897	3	AC092232	AC092232 Drosophi1	c 818	17	6.5 190523	2	BX088712	BX088712 Dantio rer
c 762	17	6.5 183190	9	AC093927	AC093927 Homo sapi	c 819	17	6.5 190629	2	AC124112	AC124112 Mus muscu
c 763	17	6.5 183558	2	AC032021	AC032021 Homo sapi	c 820	17	6.5 190708	9	AC005261	AC005261 Homo sapi
c 764	17	6.5 183684	2	AL162715	AL162715 Homo sapi	c 821	17	6.5 190798	10	AC121811	AC121811 Mus muscu
c 765	17	6.5 183707	10	AC124384	AC124384 Sus scrof	c 822	17	6.5 190842	2	AC006235	AC006235 Homo sapi
c 766	17	6.5 183772	2	AC138045	AC138045 Homo sapi	c 823	17	6.5 190952	5	BX004832	BX004832 Zebrafish
c 767	17	6.5 183807	9	AC068313	AC068313 Rattus no	c 824	17	6.5 191028	8	PU38804	PU38804 Porphyra pu
c 768	17	6.5 183855	2	AC133413	AC133413 Homo sapi	c 825	17	6.5 191116	10	AC102819	AC102819 Mus muscu
c 769	17	6.5 184396	9	AC105424	AC105424 Homo sapi	c 826	17	6.5 191255	2	AL671672	AL671672 Mouse DNA
c 770	17	6.5 184430	10	AC115811	AC115811 Mus muscu	c 827	17	6.5 191353	10	AC090320	AC090320 Homo sapi
c 771	17	6.5 184444	2	BX649509	BX649509 Homo sapi	c 828	17	6.5 191476	2	AC126104	AC126104 Rattus no
c 772	17	6.5 184635	9	AC025445	AC025445 Homo sapi	c 829	17	6.5 191603	10	AL713974	AL713974 Mouse DNA
c 773	17	6.5 184791	2	AC124360	AC124360 Mus muscu	c 830	17	6.5 191764	9	AC009506	AC009506 Homo sapi
c 774	17					c 831	17				

c 832	17	6.5 191781	10	AC124765	AC124765 Mus muscu	889	17	6.5 202374	10	AL671005	AL671005 Mouse DNA
c 833	17	6.5 191854	1	AE017156	AE017156 Haemophil	c 890	17	6.5 202565	9	AL354696	AL354696 Human DNA
c 834	17	6.5 191889	2	AC140829	AC140829 Homo sapi	c 891	17	6.5 202983	2	AC024249	AC024249 Homo sapi
c 835	17	6.5 192110	2	AP004070	AP004070 Oryza sat	c 892	17	6.5 203240	2	AC136859	AC136859 Rattus no
c 836	17	6.5 192244	2	AP001382	AP001382 Homo sapi	c 893	17	6.5 203412	2	AC092961	AC092961 Homo sapi
c 837	17	6.5 192418	2	AC147485	AC147485 Otolenur	c 894	17	6.5 204037	2	AC015881	AC015881 Homo sapi
c 838	17	6.5 193539	2	AC022190	AC022190 Homo sapi	c 895	17	6.5 204098	2	BX086705	BX086705 Homo sapi
c 839	17	6.5 193445	2	AC015951	AC015951 Homo sapi	c 896	17	6.5 204352	2	AC124526	AC124526 Mus muscu
c 840	17	6.5 193907	2	AC139762	AC139762 Mus muscu	c 897	17	6.5 204352	2	AC124526	AC124526 Mus muscu
c 841	17	6.5 193886	2	AC130783	AC130783 Pan trogl	c 898	17	6.5 204366	2	AC105639	AC105639 Rattus no
c 842	17	6.5 194437	2	AC117948	AC117948 Homo sapi	c 899	17	6.5 204937	2	AC105639	AC105639 Rattus no
c 843	17	6.5 194466	2	AL591046	AL591046 Human DNA	c 900	17	6.5 204942	2	BX530087	BX530087 Dantio rer
c 844	17	6.5 194474	2	AC137536	AC137536 Sus scrof	c 901	17	6.5 205521	2	AC146097	AC146097 Pan trogl
c 845	17	6.5 194509	8	AP001129	AP001129 Oryza sat	c 902	17	6.5 205757	10	AL844855	AL844855 Mouse DNA
c 846	17	6.5 194589	9	AC091211	AC091211 Drosophi1	c 903	17	6.5 206476	2	AC112776	AC112776 Homo sapi
c 847	17	6.5 194655	9	AC073369	AC073369 Homo sapi	c 904	17	6.5 206988	10	AL929008	AL929008 Homo sapi
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c 849	17	6.5 195007	2	AC137037	AC137037 Rattus no	c 906	17	6.5 207265	2	AC122227	AC122227 Mus muscu
c 850	17	6.5 195290	2	AL354795	AL354795 Human DNA	c 907	17	6.5 207312	10	AC110530	AC110530 Mus muscu
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c 857	17	6.5 197479	2	AL954715	AL954715 Dantio rer	c 914	17	6.5 210255	2	AC114593	AC114593 Mus muscu
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c 859	17	6.5 197721	5	AL954771	AL954771 Zebrafish	c 916	17	6.5 210754	2	AC110964	AC110964 Rattus no
c 860	17	6.5 197889	10	AC126111	AC126111 Mus muscu	c 917	17	6.5 211456	10	AL928926	AL928926 Mouse DNA
c 861	17	6.5 198269	2	AC116476	AC116476 Mus muscu	c 918	17	6.5 211602	2	AC099117	AC099117 Rattus no
c 862	17	6.5 198401	2	AC107803	AC107803 Mus muscu	c 919	17	6.5 211812	2	AC027205	AC027205 Homo sapi
c 863	17	6.5 198450	2	AC110357	AC110357 Rattus no	c 920	17	6.5 211885	2	BX005188	BX005188 Dantio rer
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c 865	17	6.5 198583	2	AC144702	AC144702 Dantio rer	c 922	17	6.5 212012	2	AC138027	AC138027 Mus muscu
c 866	17	6.5 198586	9	AC079789	AC079789 Homo sapi	c 923	17	6.5 212353	2	AC128241	AC128241 Rattus no
c 867	17	6.5 198822	2	AC110577	AC110577 Mus muscu	c 924	17	6.5 212535	2	AC128241	AC128241 Rattus no
c 868	17	6.5 199104	5	AL929266	AL929266 Zebrafish	c 925	17	6.5 212535	2	AC128241	AC128241 Rattus no
c 869	17	6.5 199199	8	ATCHRIV59	ATCHRIV59 Rattus no	c 926	17	6.5 212535	2	AC128241	AC128241 Rattus no
c 870	17	6.5 199271	2	AC142243	AC142243 Mus muscu	c 927	17	6.5 213043	2	AC130475	AC130475 Mus muscu
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c 873	17	6.5 199670	5	BX000534	BX000534 Zebrafish	c 930	17	6.5 213569	2	BX640476	BX640476 Dantio rer
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c 875	17	6.5 199908	2	AC111316	AC111316 Rattus no	c 932	17	6.5 214788	2	AC147287	AC147287 Pan trogl
c 876	17	6.5 199996	2	AC102645	AC102645 Mus muscu	c 933	17	6.5 214847	2	AC098980	AC098980 Rattus no
c 877	17	6.5 200133	2	BX510333	BX510333 Dantio rer	c 934	17	6.5 215756	10	AC087889	AC087889 Mus muscu
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c 879	17	6.5 201000	9	AC105150	AC105150 Homo sapi	c 936	17	6.5 216428	2	AC128057	AC128057 Rattus no
c 880	17	6.5 201295	2	AC128129	AC128129 Homo sapi	c 937	17	6.5 216884	2	AC134900	AC134900 Mus muscu
c 881	17	6.5 201419	10	AL808106	AL808106 Mouse DNA	c 938	17	6.5 217200	2	AC094243	AC094243 Rattus no
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c 886	17	6.5 202010	2	AC136558	AC136558 Rattus no	c 943	17	6.5 218601	2	BX649377	BX649377 Dantio rer
c 887	17	6.5 202027	2	AC120196	AC120196 Gallus ga	c 944	17	6.5 218614	2	AC123243	AC123243 Rattus no
c 888	17	6.5 202350	2	AC138257	AC138257 Mus muscu	c 945	17	6.5 219340	10	AL670771	AL670771 Mouse DNA

c 946	17	6.5	219532	2	AC125395	AC125395 Mus muscu
c 947	17	6.5	219568	10	AL844840	AL844840 Mouse DNA
c 948	17	6.5	219664	2	AC105981	AC105981 Mus muscu
c 949	17	6.5	219698	2	AC124824	AC124824 Mus muscu
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c 951	17	6.5	220528	2	AC112754	AC112754 Rattus no
c 952	17	6.5	220676	2	AC113042	AC113042 Mus muscu
c 953	17	6.5	221198	9	AP001179	AP001179 Homo sapi
c 954	17	6.5	221504	2	AC133706	AC133706 Rattus no
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c 957	17	6.5	222206	2	AC098760	AC098760 Rattus no
c 958	17	6.5	222231	2	AC130781	AC130781 Rattus no
c 959	17	6.5	222273	2	AC147053	AC147053 Mus muscu
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c 961	17	6.5	222609	2	AC096821	AC096821 Rattus no
c 962	17	6.5	222871	2	AC108094	AC108094 Homo sapi
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c 965	17	6.5	223438	2	AC137321	AC137321 Rattus no
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c 971	17	6.5	224732	2	AC103114	AC103114 Rattus no
c 972	17	6.5	224853	2	AC093610	AC093610 Rattus no
c 973	17	6.5	224910	3	AE003761	AE003761 Drosophi1
c 974	17	6.5	225011	2	AC117092	AC117092 Rattus no
c 975	17	6.5	225083	10	AL596382	AL596382 Mouse DNA
c 976	17	6.5	225267	10	AC118198	AC118198 Mus muscu
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c 978	17	6.5	226233	9	AC067717	AC067717 Homo sapi
c 979	17	6.5	226256	10	AC073599	AC073599 Mus muscu
c 980	17	6.5	226328	2	AC109575	AC109575 Rattus no
c 981	17	6.5	226351	2	AC106508	AC106508 Rattus no
c 982	17	6.5	226398	2	BX511306	BX511306 Dantio rer
c 983	17	6.5	226458	2	BX664616	BX664616 Dantio rer
c 984	17	6.5	226567	10	AC093316	AC093316 Mus muscu
c 985	17	6.5	226659	2	AC132034	AC132034 Rattus no
c 986	17	6.5	226791	2	AC094199	AC094199 Rattus no
c 987	17	6.5	226911	2	AC109717	AC109717 Rattus no
c 988	17	6.5	226929	2	BX571838	BX571838 Dantio rer
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c 990	17	6.5	227339	2	AC133408	AC133408 Rattus no
c 991	17	6.5	227350	5	AL844563	AL844563 Zebrafish
c 992	17	6.5	227791	2	AC008678	AC008678 Homo sapi
c 993	17	6.5	227849	10	AC111321	AC111321 Rattus no
c 994	17	6.5	228296	2	AL831751	AL831751 Mus muscu
c 995	17	6.5	228352	2	AC132632	AC132632 Rattus no
c 996	17	6.5	229155	9	AC018755	AC018755 Homo sapi
c 997	17	6.5	229391	2	AC105823	AC105823 Homo sapi
c 998	17	6.5	229519	2	AC095176	AC095176 Rattus no
c 999	17	6.5	229561	2	AC120067	AC120067 Rattus no
c 1000	17	6.5	229639	5	AC140947	AC140947 Gallus ga

ALIGNMENTS

RESULT 1				261 bp	DNA	linear	PAT 17-JUL-2003
BD245277	Development of novel antibiotics based on bacteriophage genomes.						
LOCUS	BD245277						
DEFINITION	Development of novel antibiotics based on bacteriophage genomes.						
ACCESSION	BD245277.1	GI:33055047					
VERSION	JP 2002531107-A/12.						
KEYWORDS	unidentified						
SOURCE	unclassified						
ORGANISM	unclassified.						
REFERENCE	1 (bases 1 to 261)						
AUTHORS	Pelletier,J., Gros,P. and Dubow,M.						
TITLE	Development of novel antibiotics based on bacteriophage genomes						
JOURNAL	Patent: JP 2002531107-A 12 24-SEP-2002;						
COMMENT	PHARTECH INC						
	OS	Staphylococcus aureus bacteriophage 77					
	PN	JP 2002531107-A/12					
	PD	24-SEP-2002					
	PF	03-DEC-1999 JP 2000585456					
	PR	03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR					
	28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR						
	01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454232 PI					JERRY	
	PELLETIER,PHILIPPE GROS,MICHAEL DUBOW						
	PC C12M15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,						
	PC C12M1/00,						
	PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC						
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Best Local Similarity	100.0%; Pred. No. 1.2e-131;						
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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RESULT 2
BD245280 297 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
DEFINITION BD245280
ACCESSION BD245280.1 GI:33055050
VERSION JP 2002531107-A/15.
KEYWORDS JP 2002531107-A/15.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 297)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 15 24-SEP-2002;
PHARTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/15
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key Location/Qualifiers
FT source 1..297
FT aureus bacteriophage 77'.
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Best Local Similarity 100.0%; Pred. No.1,28-131;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 217 TTTAACCAAGCAATAGATGATGATTGAAGAAACAGACGAAACAGACTAATT 276
QY 241 AACTAGTCATGAATGCTAG 261
DB 277 AACTAGTCATGAATGCTAG 297
RESULT 3
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
DEFINITION BD245281
ACCESSION BD245281.1 GI:33055051
VERSION JP 2002531107-A/16.
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77'.
FEATURES
Location/Qualifiers
source 1..41708

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/db_ref="taxon:32644"

Query Match 100.0%; Score 261; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 1.1e-131;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 AACTAGTCATGAATGGTAG 261
DB 29544 AACTAGTCATGAATGGTAG 29564

RESULT 4
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LOCUS AR368770
DEFINITION Sequence 3 from patent US 637652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Polletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential *Staphylococcus aureus* gene and its encoded protein
JOURNAL Patent: US 637652-A 3 23-Apr-2002;
FEATURES
Location/Qualifiers
source 1..41708
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 261; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 1.1e-131;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTAAGAAATAGCGAAATCATACGAAAAATATTCATGTTAAGGATTCATTT 60
DB 29304 ATGATTAAGAAATAGCGAAATCATACGAAAAATATTCATGTTAAGGATTCATTT 29363
QY 61 AAGCTATTCATTTAAAGGTCATATGGCATATCAATACAAATTTAAAGATGAAAC 120
DB 29364 AAGCTATTCATTTAAAGGTCATATGGCATATCAATACAAATTTAAAGATGAAAC 29423
QY 121 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTATGATGGCATCAACTTA 180
DB 29424 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTATGATGGCATCAACTTA 29483
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QY 241 AACTAGTCATGAATGGTAG 261
DB 29544 AACTAGTCATGAATGGTAG 29564

DB 29304 ATGATTAAGAAATAGCGAAATCATACGAAAAATATTCATGTTAAGGATTCATTT 29363
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DB 29484 TTTAACCAAGCATATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 29543
QY 241 AACTAGTCATGAATGGTAG 261
DB 29544 AACTAGTCATGAATGGTAG 29564

RESULT 5
AP003360 348527 bp DNA linear BCT 07-FEB-2002
LOCUS AP003360
DEFINITION *Staphylococcus aureus* subsp. *aureus* Mu50 genomic DNA, complete sequence, section 3/9.
ACCESSION AP003360 BA000017
VERSION AP003360.2 GI:14246388
KEYWORDS
SOURCE *Staphylococcus aureus* subsp. *aureus* Mu50
ORGANISM *Staphylococcus aureus* subsp. *aureus* Mu50
REFERENCE 1
AUTHORS Kuroda,M., Ohta,T., Uehiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M., Matsumaru,H., Maruyama,A., Murekami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekizawa,K., Hirakawa,H., Kubara,S., Goto,S., Yabuzaki,J., Keneshima,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramoto,K.
TITLE Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
PUBMED 11418146
REFERENCE 2 (bases 1 to 348527)
AUTHORS Ohta,T.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology, 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@tsukuba.ac.tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
COMMENT On May 29, 2001 this sequence version replaced gi:13874937.
FEATURES
Location/Qualifiers
source 1..348527
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QY 121 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTATGATGGCATCAACTTA 180
DB 29424 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTATGATGGCATCAACTTA 29483
QY 181 TTTAACCAAGCATATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 240
DB 29484 TTTAACCAAGCATATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 29543
QY 241 AACTAGTCATGAATGGTAG 261
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Db 230695 ATCATGCGAAATATTCATGTTAAGGATTCATTTAAGCTATCATTTAAAGT
230754
QY 82 CATATGGCATATCATATACAGTTAAAGATGAACAGAGTAAACATGCTAT 141
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Db 230755 CATATGGCATATCATATACAGTTAAAGATGAACAGAGTAAACATGCTAT
230814
QY 142 GTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201
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Db 230815 GTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
230874
QY 202 TGCATTGAAGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGATGATGA 253
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Db 230875 TGCATTGAAGAGACAGACAGACAGACAGACAGACAGACAGACAGATGATGA 230926
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RESULT 6
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LOCUS
DEFINITION
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sequence.
AB044534
VERSION
AB044534.1 GI:8918747
KEYWORDS
Staphylococcus aureus prophage phiPV83
SOURCE
Staphylococcus aureus prophage phiPV83
ORGANISM
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (sites)
REFERENCE
AUTHORS
TITLE
Kaneko, J., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
Panton-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
98067870
MEDLINE
PUBMED
2 (sites)
REFERENCE
AUTHORS
TITLE
Zou, D., Kaneko, J., Nerita, S. and Kamio, Y.
Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in
Staphylococcus aureus strain P83
Unpublished
3 (bases 1 to 45636)
REFERENCE
AUTHORS
TITLE
Kaneko, J., Zou, D. and Kamio, Y.
Direct Submission
Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate
School of Agricultural Science; 1-1 Tsutsumi-dori Aamimiyamachi,
Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-717-8780)

FEATURES
source
Location/Qualifiers
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QY 61 AACGATTCATTTTAAAGGTCATATGGCATATCATATACAGTTAAAGATGAAAC 120
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DB 7035 AACGATTCATTTTAAAGGTCATATGGCATATCATATACAGTTAAAGATGAAAC 7094
QY 121 GTACCATTAACATGCTTATGCTAGATGAGTAAGTACTTATGATATGGCATCA 176
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DB 7095 GTACCATTAACATGCTTATGCTAGATGAGTAAGTACTTATGATATGGCATCA 7150
RESULT 7
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS
DEFINITION
Staphylococcus aureus temperate phage phiSLT genomic DNA, complete
sequence.
ACCESSION
AB045978
VERSION
AB045978.1 GI:12697822
KEYWORDS
Staphylococcus aureus temperate phage phiSLT
SOURCE
Staphylococcus aureus temperate phage phiSLT
ORGANISM
Staphylococcus aureus temperate phage phiSLT
REFERENCE
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (sites)
Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
Phage conversion of Panton-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phiSLT.
Gene 260 (1-2), 195-206 (2001)
MEDLINE
21261956
PUBMED
11368915
TITLE
2 (bases 1 to 42942)
JOURNAL
Submitted (12-JUL-2000) Jun Kaneko, Fouchoku University, Graduate
school of Agricultural Science; 1-1 Tsutsumidori Amamiyama-cho,
Sendai, Miyagi 981-8555, Japan
AUTHORS
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-747-8780)
JOURNAL
TITLE
Direct Submission
SUBMITTER
Kaneko,J., Narita,S. and Kamio,Y.
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Query Match 61.7%; Score 161; DB 7; Length 42942;
Best Local Similarity 100.0%; Pred. No. 6,2e-77;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 ATCAATAGCGAAATATTCATGTTAAGGATTCATTTAAGCATTCATTTAAAGGT 81
DB 7294 ATCAATAGCGAAATATTCATGTTAAGGATTCATTTAAGCATTCATTTAAAGGT 7353
QY 82 CATATGGGCAATCAATACAGTTAAAGATTAACAACGTAACAATTTAAACATGCTTAT 141
DB 7354 CATATGGGCAATCAATACAGTTAAAGATTAACAACGTAACAATTTAAACATGCTTAT 7413
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DB 7414 GCGTAGATGAGATGACTTATAGATATGGCATCAAGCTTAT 7454

RESULT 8
AB009866
LOCUS
AB009866
DEFINITION
Bacteriophage phl PVL proviral DNA, complete sequence.
ACCESSION
AB009866
VERSION
AB009866.2 GI:8051698
KEYWORDS
dUTPase; sDNA binding protein; anti repressor; repressor;
integrase; luke-PV; luke-PV; holin; amidase (peptidoglycan
hydrolase); capsid protein; portal protein.
SOURCE
Staphylococcus aureus bacteriophage PVL
Staphylococcus aureus bacteriophage PVL
1 (sites)
ORGANISM
1 (sites)
REFERENCE
Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
Amino acid sequence and molecular characterization of the
complete nucleotide sequence and molecular characterization of the
temperate staphylococcal bacteriophage phlPVL carrying
Panton-Valentine leukocidin genes
JOURNAL
Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE
98067870
PUBMED
9404084
REFERENCE
2 (sites)
Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
Complete nucleotide sequence and molecular characterization of the
temperate staphylococcal bacteriophage phlPVL carrying
Panton-Valentine leukocidin genes
JOURNAL
Gene 215 (1), 57-67 (1998)
MEDLINE
98332719
PUBMED
9666077
REFERENCE
3 (bases 1 to 41401)
Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
Direct Submission
Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture; 1-1 Tsutsumi-dori
Aramiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan
(E-mail:jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)
On May 24, 2000 this sequence version replaced gi:3341907.
COMMENT
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
FEATURES
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CDS

Query Match 51.0%; Score 133; DB 7; Length 43081;
Best Local Similarity 99.5%; Pred. No. 1.3e-61;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 TATTCATTTTAAAGTCAATATGGCATATCAATCAAGTTAAAGATATGAACAAGTAC 124
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QY 125 CAATTAACATGCTTATGCGTGAATGATGACTTATGATATGCGATCAAGCTATTTTA 184
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QY 245 TAGT 248
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DB 7180 TAGT 7183

RESULT 10
AP003135/c

LOCUS AP003135 291150 bp DNA linear BCT 11-JAN-2003
DEFINITION Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
ACCSSION AP003135 BA000018
VERSION 1
KEYWORDS AP003135.2 GI:14349227
SOURCE Staphylococcus aureus subsp. aureus N315
ORGANISM Staphylococcus aureus subsp. aureus N315
REFERENCE 1
AUTHORS Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Llan,O., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kato,C.,
Sekimizu,K., Hirakawa,H., Kubara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hatori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
PUBMED 11418146
REFERENCE 2 (bases 1 to 291150)
AUTHORS Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-2001) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan
(E-mail:biocentre.go.jp, URL:htp://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT On Jun 12, 2001 this sequence version replaced gi:13701545.
FEATURES
source location/Qualifiers
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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24001 GACAGGACGACTATTATGTCATGAATGGTGG 23963

RESULT 11
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LOCUS Sequence 1209 from Patent WO02094868.
ACCESSION AX618246
VERSION AX618246.1 GI:28448442
KEYWORDS
SOURCE Staphylococcus aureus
Staphylococcus aureus
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1
AUTHORS Mastignani,V.C., Mora,M.C. and Saccarelli,M.C.
TITLE Staphylococcus aureus proteins and nucleic acids
JOURNAL Patent: WO 02094868-A 1209 28-NOV-2002;
Chiron Spa (IT)
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source Location/Qualifiers
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ORIGIN

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DB 206 ATGAATGGATTGAAGAACACAGACGAA 234

RESULT 12
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LOCUS Staphylococcus aureus phage phi 13, complete genome.
ACCESSION AF424783
VERSION AF424783.1 GI:18920591
KEYWORDS
SOURCE Staphylococcus aureus phage phi 13
ORGANISM Staphylococcus aureus phage phi 13
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
REFERENCE 1 (bases 1 to 42722)
AUTHORS Iandolo,J.J., Worrell,V., Grolicher,K.H., Qian,Y., Tian,R.,
Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and
Roe,B.A.
TITLE Comparative analysis of the genomes of the temperate bacteriophages
JOURNAL phi11, phi12 and phi13 of Staphylococcus aureus 8325
MEDLINE 22032962
PUBMED 12036589
REFERENCE 2 (bases 1 to 42722)
AUTHORS Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R.,
Lin,S. and Jia,H.
TITLE Direct Submision
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City,
OK 73190, USA
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RESULT 14
AR35085 580 bp DNA linear PAT 17-AUG-2003
LOCUS AR35085
DEFINITION Sequence 1203 from patent US 6593114.
ACCESSION AR35085
VERSION AR35085.1 GI:33761169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 580)
AUTHORS Kunach,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 1203 15-JUL-2003;
FEATURES Location/Qualifiers
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 437 ACTAATTAAGTATGATGAATGCTAG 464
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LOCUS BD245634
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245634
VERSION BD245634.1 GI:33055404
KEYWORDS JP 2002531107-A/369.
SOURCE JP 2002531107-A/369.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 43594)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
COMMENT PHAGETECH INC
OS Staphylococcus aureus bacteriophage 96
PN JP 2002531107-A/369
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
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PC A61K37/02
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FH Key Location/Qualifiers
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 5253 ACTAATTACTAGCATGAAATGCTAG 5280

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Run on: October 14, 2004, 18:55:29 ; Search time 174.116 Seconds
 (without alignments)

6368.040 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: 261
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 Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 212409041 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

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 9: geneseq12003cs:*
 10: geneseq12004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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2	261	100.0	297	3	AAA68253 Bacterioph
3	261	100.0	41708	3	AAA68247 Bacterioph
4	261	100.0	41708	4	AAAC86106 Complete
5	229	11.1	267	7	ACF72925 Staphyloc
6	28	10.7	580	2	AAV75314 Staphyloc
7	28	10.7	43576	3	AAA68609 Bacterioph

8	25	9.6	258	7	ACF73076	AcF73076 Staphyloc	c	64	16	6.1	240	7	ABZ54034	AbZ54034 Aspergill
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c	16	6.9	82588	3	AAZ22301	AAZ22301 BAC cont	c	72	16	6.1	399	6	ABL40795	ABl40795 Human pro
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c	27	6.5	623	6	ABQ31645	Abq31645 Oligonuc1	c	83	16	6.1	440	6	ABL40788	ABl40788 Human pro
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c	46	6.5	7172	2	AAV52253	AAV52253 Streptoco	c	102	16	6.1	570	4	AAH1653	AAH1653 Human cDN
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c	59	6.5	110000	8	ADA13111_1	ADa13111_1 Continuation (2 of	c	115	16	6.1	700	4	AAH93104	AAH93104 Human inf
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c 122	16	6.1	962	2	AA111883	AA111883 Probe #18	c 179	16	6.1	3879	4	AB113243	AB113243 Drosophill
c 123	16	6.1	962	4	ABA53584	ABA53584 Human foe	c 180	16	6.1	4042	5	AA583774	AA583774 DNA encod
c 124	16	6.1	962	4	AA133210	AA133210 Probe #18	c 181	16	6.1	4226	5	ABA21324	ABA21324 Human ner
c 125	16	6.1	962	4	ABA43165	ABA43165 Human bre	c 182	16	6.1	4507	4	AA103732	AA103732 Human rep
c 126	16	6.1	962	4	ABA23339	ABA23339 Probe #18	c 183	16	6.1	4507	4	ABM07913	ABM07913 Human ova
c 127	16	6.1	962	4	AAK27209	AAK27209 Human bon	c 184	16	6.1	4651	5	AA569311	AA569311 DNA encod
c 128	16	6.1	962	4	AAK01850	AAK01850 Human bra	c 185	16	6.1	4672	5	ABV25301	ABV25301 Human pro
c 129	16	6.1	962	4	AB526883	AB526883 Human liv	c 186	16	6.1	5060	10	ADE277064	ADE277064 Human cDN
c 130	16	6.1	962	5	AA101821	AA101821 Probe #18	c 187	16	6.1	5464	6	AA563343	AA563343 Chemical1
c 131	16	6.1	962	5	AB501829	AB501829 Human gen	c 188	16	6.1	5572	4	AB102646	AB102646 Drosophill
c 132	16	6.1	993	6	AB140772	AB140772 Human pro	c 189	16	6.1	5841	6	ABM92872	ABM92872 Soybean d
c 133	16	6.1	1162	3	AACT4355	AACT4355 Human sec	c 190	16	6.1	5882	4	AB112046	AB112046 Drosophill
c 134	16	6.1	1162	3	ABM07332	ABM07332 S. pneumo	c 191	16	6.1	6034	9	ABD14806	ABD14806 Human src
c 135	16	6.1	1254	7	ABK06512	ABK06512 S. pneumo	c 192	16	6.1	6061	6	AB132140	AB132140 Human tmn
c 136	16	6.1	1260	2	AA743929	AA743929 Sequence	c 193	16	6.1	6426	5	ABA20567	ABA20567 Human ner
c 137	16	6.1	1260	2	AA72049	AA72049 Sequence	c 194	16	6.1	6459	6	AB555225	AB555225 Human ner
c 138	16	6.1	1324	7	ABK07670	ABK07670 S. pneumo	c 195	16	6.1	6459	7	ABK11412	ABK11412 DNA encod
c 139	16	6.1	1488	7	ACA44808	ACA44808 Prokaryot	c 196	16	6.1	7517	4	AAK89061	AAK89061 Human dfg
c 140	16	6.1	1532	6	AB140774	AB140774 Human pro	c 197	16	6.1	7643	9	ADC30027	ADC30027 Human nov
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c 144	16	6.1	1592	6	ABK63579	ABK63579 Rat seque	c 201	16	6.1	10341	7	AB276340	AB276340 L. cupr'in
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c 146	16	6.1	1592	9	ADB79906	ADB79906 Rat beta-	c 203	16	6.1	11812	4	AA545501	AA545501 Human tmn
c 147	16	6.1	1716	4	AAH14069	AAH14069 Human cDN	c 204	16	6.1	11812	4	AA546741	AA546741 Human tmn
c 148	16	6.1	1755	7	ABT15189	ABT15189 Stephyloc	c 205	16	6.1	11812	6	AB134118	AB134118 Human tmn
c 149	16	6.1	1755	7	ACF714961	ACF714961 Patchogen	c 206	16	6.1	11812	6	ABK28431	ABK28431 DNA trans
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c 151	16	6.1	1758	4	AA554885	AA554885 Stephyloc	c 208	16	6.1	17141	6	ADN26486	ADN26486 Bovine ga
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c 153	16	6.1	1779	2	AAK20340	AAK20340 DNA encod	c 210	16	6.1	17646	7	ABT17023	ABT17023 Human sec
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c 156	16	6.1	1803	7	ADA68440	ADA68440 Streptococ	c 213	16	6.1	17646	7	ADN96997	ADN96997 Human sec
c 157	16	6.1	1932	7	ACA30294	ACA30294 Prokaryot	c 214	16	6.1	17946	4	AA536812	AA536812 Human car
c 158	16	6.1	1964	4	AAH15484	AAH15484 Human cDN	c 215	16	6.1	17946	5	ABA15608	ABA15608 Human ner
c 159	16	6.1	2000	6	AB217385	AB217385 Atebidops	c 216	16	6.1	17946	5	ABA15608	ABA15608 Human car
c 160	16	6.1	2025	7	AA587635	AA587635 L. cupr'in	c 217	16	6.1	19718	2	AAV52232	AAV52232 Streptococ
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c 163	16	6.1	2257	3	AA583773	AA583773 DNA encod	c 220	16	6.1	21521	5	ABK21357	ABK21357 Human ner
c 164	16	6.1	2307	3	AAK79656	AAK79656 Eucalyptu	c 221	16	6.1	25656	4	AB113242	AB113242 Drosophill
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c 166	16	6.1	2345	4	AAH14381	AAH14381 Human cDN	c 223	16	6.1	35425	9	ADC87616	ADC87616 Human tmn
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c 170	16	6.1	3141	7	ADA53313	ADA53313 Human cod	c 227	16	6.1	72332	8	ADN02552	ADN02552 Human WNT
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c 172	16	6.1	3212	4	AB112047	AB112047 Drosophill	c 229	16	6.1	96389	8	ADN02675	ADN02675 Mouse FN
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c 174	16	6.1	3263	4	AB125574	AB125574 Drosophill	c 231	16	6.1	96389	8	ADN02675	ADN02675 Mouse FN
c 175	16	6.1	3334	4	AB125564	AB125564 Drosophill	c 232	16	6.1	96389	8	ADN02675	ADN02675 Mouse FN
c 176	16	6.1	3637	6	AAK035236	AAK035236 Human pro	c 233	16	6.1	96389	8	ADN02675	ADN02675 Mouse FN
c 177	16	6.1	3637	9	AAK058500	AAK058500 Human RSK	c 234	16	6.1	110000	4	AAK95240_11	AAK95240_11 Continuation (12 o

c 235	16	6.1	110000	4	AAK96733_11	Continuation (12 o	c 292	15	5.7	247	4	ABS45284	Ab545284 Human liv
c 236	16	6.1	110000	6	ABR00010_11	Continuation (12 o	c 293	15	5.7	247	6	ABS19866	Ab519866 Human gen
c 237	16	6.1	110000	6	ABK08336_00	Ab408336 Human pho	c 294	15	5.7	268	5	AAK68381	AAK68381 Human lun
c 238	16	6.1	110000	6	ABA9287_0	Ab59287 Buchnera	c 295	15	5.7	268	6	ABK38292	AbK38292 cDNA erco
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c 243	16	6.1	110000	7	ABS56454_16	Continuation (17 o	c 300	15	5.7	287	7	ABK87507	ABK87507 Corn ear-
c 244	16	6.1	110000	8	ACI03408_20	Continuation (21 o	c 301	15	5.7	294	5	ABK58694	ABK58694 Human pro
c 245	16	6.1	111282	6	AAI44261	AAI44261 Human pho	c 302	15	5.7	297	6	ABS17999	ABS17999 Human gen
c 246	16	6.1	111282	6	ABS55190	ABS55190 Genomic D	c 303	15	5.7	324	6	ABD68225	ABD68225 Listeria
c 247	16	6.1	139032	6	ABO79105	Abq79105 Human for	c 304	15	5.7	325	6	AAK38836	AAK38836 Novel hum
c 248	16	6.1	139032	6	ABK03362	AbK03362 Human cDN	c 305	15	5.7	332	6	ABN18909	ABN18909 Human ORF
c 249	16	6.1	139904	9	AAH41227	AAH41227 Pyrococcu	c 306	15	5.7	334	7	AAK47653	AAK47653 Enterococ
c 250	16	6.1	349901	9	ADC86940	ADC86940 Human GPC	c 307	15	5.7	334	7	ACAI12352	ACAI12352 Prokaryot
c 251	16	6.1	349901	9	ADC86940	ADC86940 Human GPC	c 308	15	5.7	337	4	AAI88498	AAI88498 Human pol
c 252	16	6.1	349901	9	ADC86940	ADC86940 Human GPC	c 309	15	5.7	339	6	ABK78592	ABK78592 Bacillus
c 253	16	6.1	349938	9	ADC87621	ADC87621 Human GPC	c 310	15	5.7	350	7	ABK56662	ABK56662 Aspergill
c 254	15	5.7	25	7	ACF03399	ACF03399 M. gellii	c 311	15	5.7	351	2	AAQ60794	AAQ60794 Human bra
c 255	15	5.7	33	2	AAK12528	AAK12528 PCR prime	c 312	15	5.7	353	2	AAQ59515	AAQ59515 Human sec
c 256	15	5.7	47	3	AAK67197	AAK67197 Human map	c 313	15	5.7	357	3	AAK28211	AAK28211 Human sec
c 257	15	5.7	56	2	AAK76389	AAK76389 Staphyloc	c 314	15	5.7	370	7	ABK45244	ABK45244 Bovine ES
c 258	15	5.7	91	4	AAK47846	AAK47846 Enterococ	c 315	15	5.7	384	4	AAI13791	AAI13791 Probe #37
c 259	15	5.7	91	7	ACAI12573	ACAI12573 Prokaryot	c 316	15	5.7	384	4	ABK35501	ABK35501 Human foe
c 260	15	5.7	150	2	AAH86832	AAH86832 Human sin	c 317	15	5.7	384	4	AAI35151	AAI35151 Probe #38
c 261	15	5.7	152	3	AAK22270	AAK22270 Human sec	c 318	15	5.7	384	4	ABK45029	ABK45029 Human bre
c 262	15	5.7	165	4	ABA74657	ABA74657 Human foe	c 319	15	5.7	384	4	ABK25217	ABK25217 Probe #36
c 263	15	5.7	165	4	AAI55150	AAI55150 Probe #23	c 320	15	5.7	384	4	ABK29199	ABK29199 Human bon
c 264	15	5.7	165	4	AAK49303	AAK49303 Human bon	c 321	15	5.7	384	4	AAK03735	AAK03735 Human bra
c 265	15	5.7	165	4	AAK23130	AAK23130 Human bra	c 322	15	5.7	384	4	ABK28816	ABK28816 Human liv
c 266	15	5.7	165	4	ABS48942	ABS48942 Human liv	c 323	15	5.7	384	4	ABS28816	ABS28816 Human liv
c 267	15	5.7	165	6	ABS22824	ABS22824 Human gen	c 324	15	5.7	384	5	AAI03667	AAI03667 Probe #36
c 268	15	5.7	167	6	ABL78996	ABL78996 Human ova	c 325	15	5.7	384	6	ABS03751	ABS03751 Human gen
c 269	15	5.7	176	4	AAK47723	AAK47723 Enterococ	c 326	15	5.7	386	2	AAV15598	AAV15598 Papilloma
c 270	15	5.7	176	6	ACAI12419	ACAI12419 Prokaryot	c 327	15	5.7	386	2	AAV15598	AAV15598 Papilloma
c 271	15	5.7	178	6	ABZ08290	ABZ08290 Human leu	c 328	15	5.7	398	4	AAI92814	AAI92814 Human pol
c 272	15	5.7	191	4	AAK47538	AAK47538 Enterococ	c 329	15	5.7	403	2	AAQ62791	AAQ62791 Human pol
c 273	15	5.7	191	4	AAK47538	AAK47538 Enterococ	c 330	15	5.7	407	7	ABK36649	ABK36649 Bovine ES
c 274	15	5.7	191	4	AAK47538	AAK47538 Enterococ	c 331	15	5.7	414	8	ADK31018	ADK31018 DNA enco
c 275	15	5.7	191	4	AAK47538	AAK47538 Enterococ	c 332	15	5.7	423	6	ABN19543	ABN19543 Human ORF
c 276	15	5.7	191	7	ACAI12277	ACAI12277 Prokaryot	c 333	15	5.7	426	3	AAK57698	AAK57698 Aechlidon
c 277	15	5.7	191	7	ACAI12236	ACAI12236 Prokaryot	c 334	15	5.7	428	3	AAK57698	AAK57698 Aechlidon
c 278	15	5.7	191	7	ACAI12237	ACAI12237 Prokaryot	c 335	15	5.7	430	5	ABV00400	ABV00400 Human pro
c 279	15	5.7	191	7	ACAI12237	ACAI12237 Prokaryot	c 336	15	5.7	432	6	ABK76313	ABK76313 Bacillus
c 280	15	5.7	195	3	ABK14255	ABK14255 Human ova	c 337	15	5.7	433	5	ABK16674	ABK16674 Human ner
c 281	15	5.7	198	6	ABK04328	ABK04328 Human ova	c 338	15	5.7	437	5	ABK16674	ABK16674 Human ner
c 282	15	5.7	234	4	AAK02084	AAK02084 Human sec	c 339	15	5.7	438	4	AAK16674	AAK16674 Human ner
c 283	15	5.7	235	4	AAK77774	AAK77774 Human lmm	c 340	15	5.7	438	7	ACAI1657	ACAI1657 Prokaryot
c 284	15	5.7	242	6	ABK63616	ABK63616 Human lmm	c 341	15	5.7	438	7	ACAI1657	ACAI1657 Prokaryot
c 285	15	5.7	244	3	AAI10119	AAI10119 Rat liver	c 342	15	5.7	447	8	ABK48769	ABK48769 Banane ge
c 286	15	5.7	244	3	ABK48769	ABK48769 Banane ge	c 343	15	5.7	457	8	ACI26876	ACI26876 Human pan
c 287	15	5.7	247	4	ABA71289	ABA71289 Human foe	c 344	15	5.7	458	5	ABV09569	ABV09569 Human pro
c 288	15	5.7	247	4	AAI51531	AAI51531 Probe #20	c 345	15	5.7	459	5	ABV30745	ABV30745 Human pro
c 289	15	5.7	247	4	AAI51531	AAI51531 Probe #20	c 346	15	5.7	460	8	ACI25839	ACI25839 Human edu
c 290	15	5.7	247	4	AAI51531	AAI51531 Probe #20	c 347	15	5.7	460	8	ACI25839	ACI25839 Human edu
c 291	15	5.7	247	4	AAI51531	AAI51531 Probe #20	c 348	15	5.7	460	8	ACI25839	ACI25839 Human edu

c 349	15	5.7	468	ABA5855	Abz42092 Arabidops
c 350	15	5.7	468	AA138216	Abk77940 Bacillus
c 351	15	5.7	468	AAK32370	Abx12499 cDNA enco
c 352	15	5.7	468	AAK06674	Abk77941 Bacillus
c 353	15	5.7	468	AB532078	AA184272 Human pol
c 354	15	5.7	468	AB507153	AA22946 Human pro
c 355	15	5.7	478	AB505296	AA55943 Human sec
c 356	15	5.7	480	AAK79690	Abz65486 Human can
c 357	15	5.7	483	AA578335	AA11854 Aspergill
c 358	15	5.7	485	ACM14945	AcF73989 Staphyloc
c 359	15	5.7	488	ABAI6716	AA20356 Prokaryot
c 360	15	5.7	488	ABAI6715	AAK65577 Human Imm
c 361	15	5.7	488	ABAI6713	AA533230 Prokaryot
c 362	15	5.7	491	ABV99050	AA552908 Enterococ
c 363	15	5.7	492	ABJ36418	Abz4894 Oligonuc
c 364	15	5.7	493	ACC60444	Abz4895 Oligonuc
c 365	15	5.7	498	AAK94504	Abn91855 Stephyloc
c 366	15	5.7	498	AAK77857	AA22944 Human pro
c 367	15	5.7	499	ABQ57276	AA195196 Human neu
c 368	15	5.7	500	ABK53395	AAK51627 Human neu
c 369	15	5.7	506	ABV99050	AAK42653 Arabidops
c 370	15	5.7	511	AA192763	AAK43704 Sequence
c 371	15	5.7	514	ADD17902	AA297291 Human cDN
c 372	15	5.7	520	AAK39612	AA123383 Human pro
c 373	15	5.7	522	AAK62528	Abn69343 Streptococ
c 374	15	5.7	525	AAK35322	AA194407 Human neu
c 375	15	5.7	529	AAK47497	AA195446 Human neu
c 376	15	5.7	529	AAK47502	AA167694 Human neu
c 377	15	5.7	529	ABV47427	AA30332 Prokaryot
c 378	15	5.7	529	AAK12204	AA49440 Prokaryot
c 379	15	5.7	532	AAK12192	AA194407 Human neu
c 380	15	5.7	541	ABQ39476	AA56047 Human neu
c 381	15	5.7	541	ABQ39477	AA56047 Human neu
c 382	15	5.7	541	ABQ39477	AA56047 Human neu
c 383	15	5.7	551	ABK53178	AA167694 Human neu
c 384	15	5.7	567	AAK27703	AA30332 Prokaryot
c 385	15	5.7	567	ADA31675	AA49440 Prokaryot
c 386	15	5.7	569	AAK27765	AA56047 Human neu
c 387	15	5.7	570	AB113333	AA56047 Human neu
c 388	15	5.7	570	ABK59707	AA167694 Human neu
c 389	15	5.7	570	AA139572	AA30332 Prokaryot
c 390	15	5.7	570	ABK33655	AA49440 Prokaryot
c 391	15	5.7	572	AAQ44852	AA56047 Human neu
c 392	15	5.7	581	AAK10275	AA56047 Human neu
c 393	15	5.7	582	ACF73303	AA245340 Human neu
c 394	15	5.7	592	ABA62163	AA245340 Human neu
c 395	15	5.7	592	AA142117	AA245340 Human neu
c 396	15	5.7	592	AAK36383	AA245340 Human neu
c 397	15	5.7	592	AAK10484	AA245340 Human neu
c 398	15	5.7	592	ABK36058	AA245340 Human neu
c 399	15	5.7	592	ABK36058	AA245340 Human neu
c 400	15	5.7	613	ABQ66274	AA245340 Human neu
c 401	15	5.7	614	AAK66274	AA245340 Human neu
c 402	15	5.7	616	ABV51537	AA245340 Human neu
c 403	15	5.7	620	AAK98607	AA245340 Human neu
c 404	15	5.7	620	ADA68382	AA245340 Human neu
c 405	15	5.7	621	ABZ14361	AA245340 Human neu

c 463	15	5.7	1008	7	ABZ67246	Abz67246 Human sec	c 520	15	5.7	1560	6	ABZ14446	Abz14446 Arabidops
c 464	15	5.7	1008	7	ABZ73552	Abz73552 Secreted	c 521	15	5.7	1571	9	ADC85922	Adc85922 Human GPC
c 465	15	5.7	1008	7	ADC0294	Adc0294 Human sec	c 522	15	5.7	1573	3	AAZ67654	AAz67654 Human sec
c 466	15	5.7	1019	4	AAZ59766	AAz59766 Protonib	c 523	15	5.7	1581	5	AAZ73187	AAz73187 DNA encod
c 467	15	5.7	1019	7	ACF64695	Acf64695 Protonib	c 524	15	5.7	1590	6	ABA96173	ABa96173 Human imm
c 468	15	5.7	1034	2	AAZ72785	AAz72785 Metastab	c 525	15	5.7	1671	3	AAZ68002	AAz68002 Arabidops
c 469	15	5.7	1047	6	AAZ62681	AAz62681 cDNA sequ	c 526	15	5.7	1674	6	ABR83552	ABr83552 Human cDN
c 470	15	5.7	1047	8	ADZ29215	Adz29215 DNA encod	c 527	15	5.7	1674	7	ABZ71997	ABz71997 Human cDN
c 471	15	5.7	1074	7	ACA47371	Ac47371 Prokaryot	c 528	15	5.7	1695	4	AAZ30182	AAz30182 Human cDN
c 472	15	5.7	1081	7	ABX95119	Abx95119 DNA sequ	c 529	15	5.7	1695	7	ACD16622	ACd16622 Human nov
c 473	15	5.7	1082	7	ABQ79296	Abq79296 Rat blliv	c 530	15	5.7	1695	7	ACD01437	ACd01437 Human pol
c 474	15	5.7	1082	7	ADZ53527	Adz53527 Primary r	c 531	15	5.7	1695	9	AAZ62066	AAz62066 Human sec
c 475	15	5.7	1088	6	ABQ69005	Abq69005 listeria	c 532	15	5.7	1716	5	AAH52133	AAh52133 Human AFP
c 476	15	5.7	1096	2	AAZ30757	AAz30757 streptoco	c 533	15	5.7	1729	4	ABL12281	ABl12281 Drosophil
c 477	15	5.7	1107	7	ACF70527	Acf70527 Photornab	c 534	15	5.7	1809	7	ADZ52570	Adz52570 Human cod
c 478	15	5.7	1152	6	ABQ67997	Abq67997 listeria	c 535	15	5.7	1845	7	ABZ36297	ABz36297 Human sec
c 479	15	5.7	1152	6	ABQ69985	Abq69985 listeria	c 536	15	5.7	1864	3	AAZ76482	AAz76482 Human ORF
c 480	15	5.7	1188	5	AAZ87496	AAz87496 DNA encod	c 537	15	5.7	1890	4	AAZ22942	AAz22942 Human pro
c 481	15	5.7	1188	6	ABZ12826	Abz12826 Arabidops	c 538	15	5.7	1910	4	AAZ164471	AAz164471 Human car
c 482	15	5.7	1200	7	ACZ29400	Acz29400 Prokaryot	c 539	15	5.7	1936	6	ABL65828	ABl65828 Lung canc
c 483	15	5.7	1232	4	ABZ12161	Abz12161 Drosophil	c 540	15	5.7	1946	2	AAZ06796	AAz06796 Cartilage
c 484	15	5.7	1245	9	ADC91220	Adc91220 E. faecili	c 541	15	5.7	1948	6	ABQ69181	ABq69181 listeria
c 485	15	5.7	1282	2	AAZ83774	AAz83774 DNA encod	c 542	15	5.7	1968	5	AAZ66042	AAz66042 C. glutami
c 486	15	5.7	1289	4	AAZ08693	AAz08693 Rat P2-pu	c 543	15	5.7	1974	5	AAZ87504	AAz87504 DNA encod
c 487	15	5.7	1332	6	AAZ40802	AAz40802 Nucleic a	c 544	15	5.7	2000	6	ABZ15616	ABz15616 Arabidops
c 488	15	5.7	1332	6	AAZ31014	AAz31014 Yeast mev	c 545	15	5.7	2000	6	ABZ17290	ABz17290 Arabidops
c 489	15	5.7	1332	6	ABZ96800	Abz96800 S. cerevi	c 546	15	5.7	2000	6	ABZ15450	ABz15450 Arabidops
c 490	15	5.7	1345	7	ADZ71970	Adz71970 Rice gene	c 547	15	5.7	2000	6	ABZ17249	ABz17249 Arabidops
c 491	15	5.7	1367	8	AAZ61112	AAz61112 Human T81	c 548	15	5.7	2000	6	ABZ15172	ABz15172 Arabidops
c 492	15	5.7	1367	3	AAZ98043	AAz98043 Human col	c 549	15	5.7	2000	6	ABZ17176	ABz17176 Arabidops
c 493	15	5.7	1369	7	ABZ12505	Abz12505 cDNA enc	c 550	15	5.7	2000	7	ACC61839	ACc61839 Gene sequ
c 494	15	5.7	1373	3	AAZ42135	AAz42135 Arabidops	c 551	15	5.7	2000	7	ADZ72965	Adz72965 Rice gene
c 495	15	5.7	1374	7	ACZ22021	Acz22021 Prokaryot	c 552	15	5.7	2000	7	ADA69209	Ad69209 Arabidops
c 496	15	5.7	1379	3	AAZ33152	AAz33152 Arabidops	c 553	15	5.7	2000	7	ADA72698	Ad72698 Rice gene
c 497	15	5.7	1380	4	AAZ54968	AAz54968 Stephyloc	c 554	15	5.7	2000	7	ADZ69039	Adz69039 Arabidops
c 498	15	5.7	1380	4	AAZ23395	AAz23395 S. aureus	c 555	15	5.7	2003	4	ABZ119153	ABz119153 Arabidops
c 499	15	5.7	1380	7	ACZ46380	Acz46380 Prokaryot	c 556	15	5.7	2018	6	ABZ119154	ABz119154 Arabidops
c 500	15	5.7	1389	6	ABZ13553	Abz13553 Arabidops	c 557	15	5.7	2036	9	ADD69644	Ad69644 Human pol
c 501	15	5.7	1398	7	ACZ74361	Acz74361 Stephyloc	c 558	15	5.7	2036	9	ABZ06944	ABz06944 Human REM
c 502	15	5.7	1401	9	ADZ40611	Adz40611 Putative	c 559	15	5.7	2089	4	ABZ129841	ABz129841 Drosophil
c 503	15	5.7	1401	9	ADZ40629	Adz40629 Putative	c 560	15	5.7	2136	7	ABX08460	ABx08460 DNA encod
c 504	15	5.7	1420	4	ABZ17629	Abz17629 Drosophil	c 561	15	5.7	2179	4	AAZ58600	AAz58600 Human REC
c 505	15	5.7	1428	4	AAZ51247	AAz51247 Enterococ	c 562	15	5.7	2183	4	ABZ25012	ABz25012 Drosophil
c 506	15	5.7	1428	7	ACZ18357	Acz18357 Prokaryot	c 563	15	5.7	2271	3	AAZ39453	AAz39453 Arabidops
c 507	15	5.7	1431	4	AAZ53058	AAz53058 Enterococ	c 564	15	5.7	2276	4	ABZ23704	ABz23704 Arabidops
c 508	15	5.7	1443	3	AAZ35345	AAz35345 Arabidops	c 565	15	5.7	2286	6	AAZ38066	AAz38066 cDNA of n
c 509	15	5.7	1443	7	ACZ21444	Acz21444 Prokaryot	c 566	15	5.7	2400	6	AAZ32122	AAz32122 Candida a
c 510	15	5.7	1449	9	ADZ31880	Adz31880 DNA encod	c 567	15	5.7	2457	4	AAH15791	AAh15791 Human cDN
c 511	15	5.7	1455	7	ACZ61615	Acz61615 Human fat	c 568	15	5.7	2457	6	ABZ95212	ABz95212 Human rec
c 512	15	5.7	1458	2	AAZ35672	AAz35672 Glucanoba	c 569	15	5.7	2457	9	ACZ79543	ACz79543 Human met
c 513	15	5.7	1458	3	AAZ05016	AAz05016 Arabidops	c 570	15	5.7	2474	4	ABZ25010	ABz25010 Drosophil
c 514	15	5.7	1460	3	AAZ3457	AAz3457 Arabidops	c 571	15	5.7	2481	4	AAZ525945	AAz525945 Human cDN
c 515	15	5.7	1465	3	AAZ37393	AAz37393 Arabidops	c 572	15	5.7	2481	7	ABZ73286	ABz73286 Human nov
c 516	15	5.7	1477	2	AAZ69342	AAz69342 S. pneumo	c 573	15	5.7	2497	4	ABZ12037	ABz12037 Drosophil
c 517	15	5.7	1491	6	ABZ67918	ABz67918 streptoco	c 574	15	5.7	2499	7	ACZ29300	ACz29300 Prokaryot
c 518	15	5.7	1501	6	AAZ42330	AAz42330 Agrocyphe	c 575	15	5.7	2541	4	ABZ27442	ABz27442 Drosophil
c 519	15	5.7	1501	2	AAZ27424	AAz27424 A. pedicel	c 576	15	5.7	2570	4	ABZ13332	ABz13332 Drosophil

c 577	15	5.7	2598	4	AA164986	AA164986	Mortellella
c 578	15	5.7	2604	4	AAH15797	AAH15797	Human cDN
c 579	15	5.7	2631	3	AA992471	AA992471	Shewanella
c 580	15	5.7	2652	3	AAA15173	AAA15173	V. marinus
c 581	15	5.7	2672	4	ABL23702	ABL23702	Drosophila
c 582	15	5.7	2678	9	ADBE2602	ADBE2602	Human cDN
c 583	15	5.7	2680	4	AAH16335	AAH16335	Human cDN
c 584	15	5.7	2689	6	ABU41575	ABU41575	Human cDN
c 585	15	5.7	2711	3	AAA48642	AAA48642	Rat Mp-10
c 586	15	5.7	2725	6	ABK35276	ABK35276	Human cDN
c 587	15	5.7	2742	9	ADCG0986	ADCG0986	E. faeculi
c 588	15	5.7	2769	6	AB211334	AB211334	Human pol
c 589	15	5.7	2776	5	ABA20040	ABA20040	Human ner
c 590	15	5.7	2840	4	AAH14222	AAH14222	Human cDN
c 591	15	5.7	2840	6	ABU3518	ABU3518	Human rec
c 592	15	5.7	2840	6	ABA95211	ABA95211	Human mel
c 593	15	5.7	2840	9	ACF79542	ACF79542	Human tra
c 594	15	5.7	2841	2	AAV74488	AAV74488	Staphyloc
c 595	15	5.7	2844	4	ABL22730	ABL22730	Drosophila
c 596	15	5.7	2853	7	ACA37230	ACA37230	Prokaryot
c 597	15	5.7	2860	4	AAH42602	AAH42602	Nucleotid
c 598	15	5.7	2872	2	AAQ21001	AAQ21001	Murline re
c 599	15	5.7	2872	2	AAI36881	AAI36881	Murline re
c 600	15	5.7	2872	2	AAK29853	AAK29853	Mouse rec
c 601	15	5.7	2881	4	AAK27019	AAK27019	cDNA enco
c 602	15	5.7	2881	9	ADB93197	ADB93197	Human cDN
c 603	15	5.7	2942	7	ADA53471	ADA53471	Human cod
c 604	15	5.7	3021	4	AAH52380	AAH52380	S. epider
c 605	15	5.7	3034	6	ABQ14764	ABQ14764	Oligonuc
c 606	15	5.7	3034	6	ABQ14765	ABQ14765	Oligonuc
c 607	15	5.7	3081	2	AAI67442	AAI67442	H. pylori
c 608	15	5.7	3098	4	ABL28340	ABL28340	Drosophila
c 609	15	5.7	3125	9	ADBS8074	ADBS8074	Human gen
c 610	15	5.7	3125	9	ADBS8070	ADBS8070	Human gen
c 611	15	5.7	3129	7	ACF03435	ACF03435	Mycoplasma
c 612	15	5.7	3148	4	AAH54695	AAH54695	S. epider
c 613	15	5.7	3148	6	ABQ70799	ABQ70799	Listeria
c 614	15	5.7	3173	4	AAH54390	AAH54390	S. epider
c 615	15	5.7	3199	5	AAH67511	AAH67511	DNA enco
c 616	15	5.7	3213	5	AAH65545	AAH65545	DNA enco
c 617	15	5.7	3251	4	ABL03846	ABL03846	Drosophila
c 618	15	5.7	3270	4	ABL27756	ABL27756	Drosophila
c 619	15	5.7	3278	7	ACC00397	ACC00397	Human cel
c 620	15	5.7	3295	4	AAH36186	AAH36186	Human car
c 621	15	5.7	3295	9	AAK71764	AAK71764	Human imm
c 622	15	5.7	3295	9	AAH46680	AAH46680	Human car
c 623	15	5.7	3308	3	AAA26917	AAA26917	Essential
c 624	15	5.7	3308	4	AAH91599	AAH91599	Staphyloc
c 625	15	5.7	3308	4	AAH08068	AAH08068	Staphyloc
c 626	15	5.7	3308	9	ADH67446	ADH67446	Antibacte
c 627	15	5.7	3308	9	AAH673670	AAH673670	Mutant ba
c 628	15	5.7	3344	4	AAH54738	AAH54738	S. epider
c 629	15	5.7	3368	5	AAH55563	AAH55563	DNA enco
c 630	15	5.7	3373	6	ABV99388	ABV99388	Human NOV
c 631	15	5.7	3410	4	ABU18618	ABU18618	Drosophila
c 632	15	5.7	3440	7	AB224210	AB224210	Human SLC
c 633	15	5.7	3481	7	AB242407	AB242407	Human SLC
c 634	15	5.7	3492	4	AAU04161	AAU04161	Human rep
c 635	15	5.7	3526	6	ABQ61182	ABQ61182	FLJ20047
c 636	15	5.7	3545	4	AAH25965	AAH25965	Human cDN
c 637	15	5.7	3545	7	ABK73306	ABK73306	Human nov
c 638	15	5.7	3562	4	ABU06749	ABU06749	Drosophila
c 639	15	5.7	3594	7	ACA20853	ACA20853	Prokaryot
c 640	15	5.7	3639	4	AAH51721	AAH51721	Staphyloc
c 641	15	5.7	3651	7	ACF74791	ACF74791	Staphyloc
c 642	15	5.7	3652	4	ABU16754	ABU16754	Drosophila
c 643	15	5.7	3654	4	AAH54788	AAH54788	Staphyloc
c 644	15	5.7	3654	7	ABU15084	ABU15084	Pathogen
c 645	15	5.7	3654	7	ACA19742	ACA19742	Prokaryot
c 646	15	5.7	3658	4	AAH17782	AAH17782	Drosophila
c 647	15	5.7	3666	4	AAH54179	AAH54179	S. epider
c 648	15	5.7	3672	7	ACA46452	ACA46452	Prokaryot
c 649	15	5.7	3674	6	ABH57736	ABH57736	cDNA enco
c 650	15	5.7	3754	2	AAV74869	AAV74869	Staphyloc
c 651	15	5.7	3809	4	AAH10069	AAH10069	Drosophila
c 652	15	5.7	3870	4	AAH84271	AAH84271	Human imm
c 653	15	5.7	3934	2	AAI97233	AAI97233	Trimmed e
c 654	15	5.7	4020	7	AB224206	AB224206	Human SLC
c 655	15	5.7	4034	4	ABU03372	ABU03372	Drosophila
c 656	15	5.7	4038	4	ABU29090	ABU29090	Drosophila
c 657	15	5.7	4116	6	ABK24522	ABK24522	EIF-2alpha
c 658	15	5.7	4125	4	AAH84261	AAH84261	Human imm
c 659	15	5.7	4129	4	AAH84261	AAH84261	Human imm
c 660	15	5.7	4200	4	ABU17628	ABU17628	Drosophila
c 661	15	5.7	4204	4	ABU12160	ABU12160	Drosophila
c 662	15	5.7	4327	6	ABH56408	ABH56408	Human DNA
c 663	15	5.7	4361	5	AAH84867	AAH84867	DNA enco
c 664	15	5.7	4398	3	AAH43063	AAH43063	Abi1dops
c 665	15	5.7	4409	6	ABK89163	ABK89163	cDNA enco
c 666	15	5.7	4441	3	AAA47759	AAA47759	RIAA0160
c 667	15	5.7	4441	6	ABH69961	ABH69961	Penicreas
c 668	15	5.7	4441	6	ABH69961	ABH69961	Penicreas
c 669	15	5.7	4455	4	ABU03329	ABU03329	Drosophila
c 670	15	5.7	4465	6	ABH77932	ABH77932	Hypoxia-r
c 671	15	5.7	4465	7	ABH08805	ABH08805	Angiogene
c 672	15	5.7	4465	8	ACC57774	ACC57774	Human cyc
c 673	15	5.7	4465	9	ACF79931	ACF79931	Breast ca
c 674	15	5.7	4466	7	ACA03925	ACA03925	cDNA down
c 675	15	5.7	4496	7	ABH63478	ABH63478	Human cDN
c 676	15	5.7	4582	4	AAK72026	AAK72026	Human imm
c 677	15	5.7	4594	2	AAV74511	AAV74511	Staphyloc
c 678	15	5.7	4623	4	ABU12280	ABU12280	Drosophila
c 679	15	5.7	4750	9	ADH25722	ADH25722	Human cDN
c 680	15	5.7	4802	7	ABH68141	ABH68141	Human sec
c 681	15	5.7	4802	7	ABH74620	ABH74620	Secreted
c 682	15	5.7	4802	9	ADH21011	ADH21011	Human sec
c 683	15	5.7	4910	4	ABU12036	ABU12036	Drosophila
c 684	15	5.7	4997	7	ACA47636	ACA47636	Prokaryot
c 685	15	5.7	4998	4	AAH65573	AAH65573	Human imm
c 686	15	5.7	5082	6	ABH70953	ABH70953	Listeria
c 687	15	5.7	5151	4	ABU29840	ABU29840	Drosophila
c 688	15	5.7	5251	4	ABU15640	ABU15640	DNA enco
c 689	15	5.7	5251	4	AAH57144	AAH57144	Drosophila
c 690	15	5.7	5251	9	ADH35857	ADH35857	Drosophila

691	15	5.7	5373	4	ABU16748	AbU16748 Drosophila	748	15	5.7	10207	7	AAU51838	AAU51838 Stephyloc
692	15	5.7	5356	4	ABU09460	AbU09460 Drosophila	749	15	5.7	10207	7	ABZ77350	ABZ77350 Nucleotid
693	15	5.7	5721	6	ABG71037	AbG71037 listeria	750	15	5.7	10267	6	ABV99390	ABV99390 Human NOV
694	15	5.7	5740	3	AAA61521	AAa61521 A. vitis	751	15	5.7	10280	4	ABU17233	ABU17233 Drosophila
695	15	5.7	5740	3	AAA61522	AAa61522 A. vitis	752	15	5.7	10382	4	AAK67484	AAK67484 Human
696	15	5.7	5758	6	ABU32660	AbU32660 Human	753	15	5.7	10487	4	ABU13186	ABU13186 Drosophila
697	15	5.7	5798	6	ABU33666	AbU33666 Human	754	15	5.7	10945	6	ABR28333	ABR28333 DNA trans
698	15	5.7	5885	4	ABU28882	AbU28882 Drosophila	755	15	5.7	10963	4	ABU09896	ABU09896 Drosophila
699	15	5.7	5966	2	AAV74333	AAv74333 Stephyloc	756	15	5.7	11327	4	ADA20274	ADA20274 Human cyc
700	15	5.7	6042	6	AAU33945	AAu33945 Human	757	15	5.7	11327	4	AAU54632	AAU54632 Human
701	15	5.7	6056	4	AAU46363	AAu46363 Tumour su	758	15	5.7	11715	1	AAU81564	AAU81564 Tumour su
702	15	5.7	6056	6	ABU32780	AbU32780 Human	759	15	5.7	11724	1	AAU70102	AAU70102 Compelte
703	15	5.7	6123	6	ABU33036	AbU33036 Human	760	15	5.7	11724	4	AAU57497	AAU57497 Human liv
704	15	5.7	6796	4	ABU04318	AbU04318 Drosophila	761	15	5.7	11725	2	AAU32796	AAU32796 Human pro
705	15	5.7	7040	7	ABU09900	AbU09900 Human	762	15	5.7	11725	2	AAU79723	AAU79723 Human pro
706	15	5.7	7040	9	ABU09900	AbU09900 Human	763	15	5.7	11725	2	AAU32179	AAU32179 Human pro
707	15	5.7	7080	4	ABU10068	AbU10068 Drosophila	764	15	5.7	11725	4	AAU54051	AAU54051 Human pro
708	15	5.7	7116	4	ABU03328	AbU03328 Drosophila	765	15	5.7	11725	5	AAU87514	AAU87514 DNA encod
709	15	5.7	7143	4	ABU06748	AbU06748 Drosophila	766	15	5.7	11802	2	AAU74381	AAU74381 Stephyloc
710	15	5.7	7143	6	ABU32983	AbU32983 Human	767	15	5.7	12509	4	ABU19152	ABU19152 Drosophila
711	15	5.7	7320	6	AAU68081	AAu68081 H. pylori	768	15	5.7	13292	4	ABU17232	ABU17232 Drosophila
712	15	5.7	7346	6	ABU32344	AbU32344 Human	769	15	5.7	13376	6	ABU32582	ABU32582 Human
713	15	5.7	7490	6	ABU32282	AbU32282 Human	770	15	5.7	13784	6	ABU40062	ABU40062 Human
714	15	5.7	7494	2	AAU74380	AAu74380 Stephyloc	771	15	5.7	13798	4	ABU08500	ABU08500 Human
715	15	5.7	7599	4	AAU04162	AAu04162 Human	772	15	5.7	13860	7	ACU44867	ACU44867 Human
716	15	5.7	7681	6	ABU31026	AbU31026 Operon D	773	15	5.7	13878	9	ADC01230	ADC01230 Human
717	15	5.7	7693	6	ABU31023	AbU31023 Operon A	774	15	5.7	13917	6	ADC01037	ADC01037 Human
718	15	5.7	7693	6	ABU31024	AbU31024 Operon B	775	15	5.7	13965	8	ADC019035	ADC019035 Human
719	15	5.7	7876	4	ABU03166	AbU03166 Drosophila	776	15	5.7	14024	4	AAU36381	AAU36381 Human
720	15	5.7	8054	2	AAU88825	AAu88825 Candida	777	15	5.7	14024	5	AAU330157	AAU330157 Human
721	15	5.7	8224	6	ABU31027	AbU31027 Operon E	778	15	5.7	14024	9	ABU33494	ABU33494 Human
722	15	5.7	8235	6	ABU31025	AbU31025 Operon C	779	15	5.7	14024	9	ABU33494	ABU33494 Human
723	15	5.7	8400	6	ABU31029	AbU31029 Operon G	780	15	5.7	14124	5	ABU15503	ABU15503 Human
724	15	5.7	8635	4	ABU79024	ABu79024 E. coli	781	15	5.7	14156	7	ACU64518	ACU64518 Human
725	15	5.7	8643	4	ABU88854	ABu88854 Escherich	782	15	5.7	14156	7	ACU64518	ACU64518 Human
726	15	5.7	8734	4	AAU72027	AAu72027 Human	783	15	5.7	14171	7	AAU37152	AAU37152 Human
727	15	5.7	8776	6	ABU40067	AbU40067 Human	784	15	5.7	14171	7	ABU60140	ABU60140 Human
728	15	5.7	8790	9	ADD13780	AdU13780 Plasmid P	785	15	5.7	14483	7	ACC48945	ACC48945 Escherich
729	15	5.7	9005	4	ABU29370	AbU29370 Drosophila	786	15	5.7	14623	6	ADD31039	ADD31039 Plasmid
730	15	5.7	9015	6	ABU70188	AbU70188 Chromosom	787	15	5.7	14623	6	ADD31041	ADD31041 Plasmid
731	15	5.7	9015	6	AAU61138	AAu61138 Human	788	15	5.7	15240	3	AAU34995	AAU34995 Human
732	15	5.7	9159	5	AAU87481	AAu87481 DNA encod	789	15	5.7	15240	3	AAU34995	AAU34995 Human
733	15	5.7	9193	6	ABU99389	AbU99389 Human	790	15	5.7	15240	7	ABU26811	ABU26811 Human
734	15	5.7	9212	2	AAU13271	AAu13271 Enterococ	791	15	5.7	15405	4	ABU03146	ABU03146 Human
735	15	5.7	9212	6	ABU99066	AbU99066 Enterococ	792	15	5.7	15933	4	ABU30408	ABU30408 Human
736	15	5.7	9263	4	ABU15172	AbU15172 Drosophila	793	15	5.7	15933	4	ABU06114	ABU06114 Human
737	15	5.7	9451	6	ABU97450	AbU97450 Human	794	15	5.7	15998	4	AAU37153	AAU37153 Human
738	15	5.7	9453	3	AAA34894	AAa34894 Human	795	15	5.7	15998	7	ABU60141	ABU60141 Human
739	15	5.7	9453	3	AAU21116	AAu21116 Human	796	15	5.7	17727	5	AAU87482	AAU87482 Human
740	15	5.7	9453	6	ABU65014	AbU65014 Lung can	797	15	5.7	18488	6	ABU14444	ABU14444 Human
741	15	5.7	9453	6	ABU84194	AbU84194 Human	798	15	5.7	18877	4	AAU28632	AAU28632 Human
742	15	5.7	9453	6	ABU96610	AbU96610 Human	799	15	5.7	19191	4	AAU67485	AAU67485 Human
743	15	5.7	9680	4	ABU20930	AbU20930 Human	800	15	5.7	19227	2	AAU81944	AAU81944 Human
744	15	5.7	9814	3	AAU79596	AAu79596 Virulence	801	15	5.7	19227	2	AAU81944	AAU81944 Human
745	15	5.7	9814	6	ABU83473	AbU83473 Pasteurel	802	15	5.7	19738	6	ABU01436	ABU01436 Human
746	15	5.7	9859	6	ABU34133	AbU34133 Human	803	15	5.7	19861	5	AAU87516	AAU87516 Human
747	15	5.7	10207	2	AAU53134	AAu53134 Stephyloc	804	15	5.7	20776	4	ABU30040	ABU30040 Human

805	15	5.7	21708	AB114604	Drosophil	Ab114604 Drosophil	c 862	15	5.7	96599	9	ABM72650	Human JAK	AbM72650 Human JAK
c 806	15	5.7	21724	AA526629	Human gen	AA526629 Human gen	c 863	15	5.7	96596	9	ADCS287	Mouse Fls	ADCS287 Mouse Fls
c 807	15	5.7	21724	AAK61625	Human Imm	AAK61625 Human Imm	c 864	15	5.7	96597	8	ADAO2807	Mouse Fls	ADAO2807 Mouse Fls
c 808	15	5.7	21724	ABK73978	Human nov	ABK73978 Human nov	c 865	15	5.7	96599	8	ADB72545	Mouse Fls	ADB72545 Mouse Fls
c 809	15	5.7	21727	AA526630	Human gen	AA526630 Human gen	c 866	15	5.7	96599	8	ADAO2747	Mouse Ifr	ADAO2747 Mouse Ifr
c 810	15	5.7	21727	AAK61626	Human Imm	AAK61626 Human Imm	c 867	15	5.7	96599	8	ADB72485	Mouse Ifr	ADB72485 Mouse Ifr
c 811	15	5.7	21727	AAK73979	Human nov	AAK73979 Human nov	c 868	15	5.7	96599	9	ADCS2227	Mouse Ifr	ADCS2227 Mouse Ifr
c 812	15	5.7	22875	AA128694	Human	AA128694 Human	c 869	15	5.7	96649	7	ACC5150	Mouse Ifr	ACC5150 Mouse Ifr
c 813	15	5.7	23821	AAK92469	Shevnaell	AAK92469 Shevnaell	c 870	15	5.7	96690	6	ABK12169	Human DNA	ABK12169 Human DNA
c 814	15	5.7	24099	AA106944	Human rep	AA106944 Human rep	c 871	15	5.7	109201	6	ABO68125	Human cont	ABO68125 Human cont
c 816	15	5.7	25359	ACF63588_12	Continuatio	Continuatio (13 o	c 872	15	5.7	110000	2	AAV21209	10	Continuatio (11 o
c 816	15	5.7	27425	3	AA53978	Continuatio (13 o	c 873	15	5.7	110000	2	AAV21209	12	Continuatio (11 o
c 817	15	5.7	28091	4	AAK73432	Human Imm	c 874	15	5.7	110000	2	AAV21209	13	Continuatio (14 o
c 818	15	5.7	28091	5	ABAI5375	Human nov	c 875	15	5.7	110000	2	AAZ01425	102	Continuatio (3 o
c 819	15	5.7	28120	4	AAK77434	Human Imm	c 876	15	5.7	110000	4	AAK93240	07	Continuatio (8 o
c 820	15	5.7	28120	5	ABAI5379	Human nov	c 877	15	5.7	110000	4	AAK96733	07	Continuatio (8 o
c 821	15	5.7	28526	9	ADDA7028	Human gen	c 878	15	5.7	110000	6	ABN71527	10	Continuatio (11 o
c 822	15	5.7	30037	5	ABAI20038	Human nov	c 879	15	5.7	110000	6	ABFO0010	07	Continuatio (8 o
c 823	15	5.7	32132	4	AA135943	Human mus	c 880	15	5.7	110000	6	ABX08336	02	Continuatio (3 o
c 824	15	5.7	32132	4	AA107060	Human rep	c 881	15	5.7	110000	6	ABX09521	07	Continuatio (8 o
c 825	15	5.7	32132	7	ABX58931	cDNA enco	c 882	15	5.7	110000	6	ABX0521_13	0	Continuatio (14 o
c 826	15	5.7	32200	8	ABK42817	Genomic s	c 883	15	5.7	110000	6	ABX0521_13	0	Continuatio (14 o
c 827	15	5.7	32200	8	AD61073	Connectiv	c 884	15	5.7	110000	6	ABO69245	10	Continuatio (15 o
c 828	15	5.7	32768	2	AAK13065	Enterococ	c 885	15	5.7	110000	6	ABO67197	08	Continuatio (9 o
c 829	15	5.7	32768	6	AB598860	Enterococ	c 886	15	5.7	110000	6	ABO67197	08	Continuatio (10 o
c 830	15	5.7	34750	4	AB116322	Drosophil	c 887	15	5.7	110000	6	ABFO1503	07	Continuatio (10 o
c 831	15	5.7	39651	4	AB118856	Drosophil	c 888	15	5.7	110000	6	ABO30341_00	0	Continuatio (8 o
c 832	15	5.7	40138	2	AAV01946	V. marinu	c 889	15	5.7	110000	6	ABO30341_00	0	Continuatio (10 o
c 833	15	5.7	40138	3	AAK71520	V. marinu	c 890	15	5.7	110000	6	ABO30341_04	07	Continuatio (5 o
c 834	15	5.7	41104	6	AAO36260	Human G-P	c 891	15	5.7	110000	6	ABO30341_11	0	Continuatio (8 o
c 835	15	5.7	41587	4	AA164984	Moritella	c 892	15	5.7	110000	6	ABO30341_11	0	Continuatio (12 o
c 836	15	5.7	47108	6	ABK31511	Signal tr	c 893	15	5.7	110000	7	ACF67367_01	0	Continuatio (12 o
c 837	15	5.7	49984	6	ABD44995	Human tra	c 894	15	5.7	110000	7	ACF67367_01	0	Continuatio (12 o
c 838	15	5.7	5385	2	AAK20251	Borrelia	c 895	15	5.7	110000	7	ACF67367_36	0	Continuatio (37 o
c 839	15	5.7	54663	4	AAK60625	Human Imm	c 896	15	5.7	110000	7	ACF67367_30	0	Continuatio (51 o
c 840	15	5.7	54877	7	ABK6026	Human Imm	c 897	15	5.7	110000	7	ACF65387_1	0	Continuatio (12 o
c 841	15	5.7	54877	7	ABK67791	Human sec	c 898	15	5.7	110000	7	ACF65388_11	0	Continuatio (12 o
c 842	15	5.7	54877	7	ABK74225	Secreted	c 899	15	5.7	110000	7	ACF65388_11	0	Continuatio (12 o
c 843	15	5.7	54877	7	ADA98754	Human sec	c 900	15	5.7	110000	7	ACF65388_11	0	Continuatio (12 o
c 844	15	5.7	56153	3	AA546793	Tumour su	c 901	15	5.7	110000	7	AAZ03223_1	0	Continuatio (12 o
c 845	15	5.7	56583	3	AAK315003	Human ade	c 902	15	5.7	114793	4	AAAD088215	0	Continuatio (12 o
c 846	15	5.7	56583	3	AAK21125	Human	c 903	15	5.7	118584	9	ABK937623	0	Continuatio (12 o
c 847	15	5.7	56583	7	ABZ96819	Human low	c 904	15	5.7	128600	6	ABK937623	0	Continuatio (12 o
c 848	15	5.7	56866	4	AB118488	Human nuc	c 905	15	5.7	128600	6	ABK937623	0	Continuatio (12 o
c 849	15	5.7	58181	7	ABZ68140	Human sec	c 906	15	5.7	128600	6	ABK937623	0	Continuatio (12 o
c 850	15	5.7	58181	7	ABZ74619	Secreted	c 907	15	5.7	148567	8	ACA62841	0	Continuatio (12 o
c 851	15	5.7	58181	9	ADK21010	Human sec	c 908	15	5.7	148567	8	ACA62841	0	Continuatio (12 o
c 852	15	5.7	58407	2	AAV21210	Human sec	c 909	15	5.7	156638	6	ABO618850	0	Continuatio (12 o
c 853	15	5.7	65654	4	AAK66282	Human Imm	c 910	15	5.7	180557	6	ABN853780	0	Continuatio (12 o
c 854	15	5.7	69173	8	ADAO2942	Human Imm	c 911	15	5.7	185695	7	ABQ77405	0	Continuatio (12 o
c 855	15	5.7	69173	9	ADK72680	Human TLE	c 912	15	5.7	185695	7	ABQ77405	0	Continuatio (12 o
c 856	15	5.7	69173	9	ADK85422	Human TLE	c 913	15	5.7	199377	9	ADCS3071	0	Continuatio (12 o
c 857	15	5.7	90091	9	ADCS8509	Mouse mCG	c 914	15	5.7	222880	9	ADCS7622	0	Continuatio (12 o
c 858	15	5.7	90100	8	ADCS3029	Mouse mCG	c 915	15	5.7	266685	6	AB556563	0	Continuatio (12 o
c 859	15	5.7	90100	9	ADK72767	Mouse mCG	c 916	15	5.7	325791	4	AAK313104	0	Continuatio (12 o
c 860	15	5.7	96587	9	ADK85392	Human JAK	c 917	15	5.7	349881	9	ADCS6642	0	Continuatio (12 o
c 861	15	5.7	96589	8	ADK02912	Human JAK	c 918	15	5.7	349980	6	ABO618844	0	Continuatio (12 o

c 919 14 5.4 24 3 AAC73253
c 920 14 5.4 24 6 ABs61668
c 921 14 5.4 25 4 AAF58028
c 922 14 5.4 25 8 ACI70181
c 923 14 5.4 25 8 ACI25258
c 924 14 5.4 29 2 AAT63585
c 925 14 5.4 29 3 AAA26841
c 926 14 5.4 33 6 AAI19219
c 927 14 5.4 42 3 AAC73255
c 928 14 5.4 47 3 AAZ66448
c 929 14 5.4 51 4 AAL30743
c 930 14 5.4 51 4 ABL30744
c 931 14 5.4 51 5 ABL00943
c 932 14 5.4 51 5 ABL00061
c 933 14 5.4 60 6 ABN46607
c 934 14 5.4 70 2 AAI12874
c 935 14 5.4 70 2 AAI11711
c 936 14 5.4 80 2 AAQ33826
c 937 14 5.4 90 8 AOC70036
c 938 14 5.4 98 7 ACC49875
c 939 14 5.4 98 9 ADE27712
c 940 14 5.4 103 6 ABK45891
c 941 14 5.4 105 8 ADA73772
c 942 14 5.4 105 8 ADA02219
c 943 14 5.4 105 8 ADB71958
c 944 14 5.4 106 8 ADN02226
c 945 14 5.4 106 9 ADB71965
c 946 14 5.4 118 3 AAC25924
c 947 14 5.4 120 3 AAA26772
c 948 14 5.4 136 3 AAC05487
c 949 14 5.4 140 8 ACH31705
c 950 14 5.4 143 2 AAI10604
c 951 14 5.4 151 4 AAI37063
c 952 14 5.4 163 4 AAL24209
c 953 14 5.4 169 5 ABV60150
c 954 14 5.4 174 7 ABK86363
c 955 14 5.4 176 2 AAV86898
c 956 14 5.4 178 4 AAI26036
c 957 14 5.4 178 4 AAI73194
c 958 14 5.4 178 4 ABA38633
c 959 14 5.4 178 4 AAI53623
c 960 14 5.4 178 4 AAI47794
c 961 14 5.4 178 4 AAI21629
c 962 14 5.4 178 4 ABA47519
c 963 14 5.4 178 6 ABA25883
c 964 14 5.4 178 6 ABA21804
c 965 14 5.4 187 6 ABA62833
c 966 14 5.4 188 2 AAT21028
c 967 14 5.4 189 3 AAC27854
c 968 14 5.4 194 7 ACD94370
c 969 14 5.4 195 6 ABA91231
c 970 14 5.4 200 6 ABG73052
c 971 14 5.4 203 3 AAC26282
c 972 14 5.4 204 7 ABA259063
c 973 14 5.4 204 8 ADA32410
c 974 14 5.4 205 3 AAC30061
c 975 14 5.4 209 7 ACD92334

Aac73253 Forward P
AbS61668 Analyte s
AaF58028 Tempso
AcI70181 Human mic
AcI25258 Human mic
AaF63585 PCR prime
AaZ66448 Trichospo
AaI19219 Kringle P
Aac73255 Single ba
AaZ66448 Human map
AaI30743 Human SNP
AaI30744 Human SNP
AbI00943 Human aml
AbI00061 Human sll
AbH46607 Human spl
AaI12874 Human bla
AaI1711 Human bla
AaQ33826 Domstre
Aac70036 PCR prime
Acc49875 Synthetic
Ade27712 ActI-CCR4
AbK45891 cDNA enco
Ada73772 Carcinoma
Ada02219 Mouse car
AdH71958 Mouse car
Adn02226 Mouse car
Adb71965 Mouse car
Aac25924 Human sec
AaZ6772 Trichospo
Aac05487 Human sec
Ach31705 Human bon
AaI10604 Human col
AaI37063 Human col
AaI24209 Human bre
Abv60150 Human pro
AbK86363 Corn ear-
AaV86898 EST clone
AaI26036 Probe #15
Aba73194 Human toe
AaI53623 Probe #22
AaK47794 Human bon
AaI21629 Human bra
AbH47519 Human liv
AbH25883 Human ORF
Aba21804 Human gen
Aba62833 Human can
AaI21028 Human gen
Aac27854 Human sec
Acd94370 Human col
AbH91231 StephyLoc
AbG73052 Human GPR
Aac26282 Human sec
AbS59063 Hyperperns
Ada32410 DNA enco
Aac30061 Human sec
Acd92334 Human col

976 14 5.4 210 6 ABA91585
c 977 14 5.4 213 4 AAS30318
c 978 14 5.4 213 4 AAL01999
c 979 14 5.4 225 6 ABA77100
c 980 14 5.4 228 2 AAI13874
c 981 14 5.4 228 6 ABA99669
c 982 14 5.4 230 4 AAK61368
c 983 14 5.4 234 3 AAC16103
c 984 14 5.4 234 3 AAC28915
c 985 14 5.4 240 3 AAC02395
c 986 14 5.4 240 6 ABA20425
c 987 14 5.4 240 7 ABA269409
c 988 14 5.4 246 4 AAS49115
c 989 14 5.4 246 4 AAK79929
c 990 14 5.4 246 7 AAI16353
c 991 14 5.4 248 3 AAC02463
c 992 14 5.4 250 4 AAI33619
c 993 14 5.4 251 2 AAI12579
c 994 14 5.4 251 3 AAC27012
c 995 14 5.4 255 5 AAB82022
c 996 14 5.4 262 5 ABA15216
c 997 14 5.4 262 6 ABA166051
c 998 14 5.4 262 6 ABA167339
c 999 14 5.4 263 3 AAC12015
1000 14 5.4 263 8 ACH21976

ALIGNMENTS

RESULT 1
AAA68250
ID AAA68250 standard; DNA; 261 BP.
XX
AC AAA68250;
XX
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
XX 27-OCT-2000 (first entry)
DE Bacteriophage 77 77ORF043 nucleotide sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
XX bacterial growth inhibition; bacterial infection; ds.
XX
XX Staphylococcus aureus; bacteriophage 77.
OS
XX
XX WO200032825-A2.
XX
XX
XX 08-JUN-2000.
XX
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX
XX 03-DEC-1998; 98US-0110992P.
XX 03-JUN-1999; 99US-00326144.
XX 28-SEP-1999; 99US-00407804.
XX 30-SEP-1999; 99US-0157218P.

Abn91585 StephyLoc
Aas30318 DNA enco
AaI01999 Human rep
Aba77100 Human ORF
AaI13874 Enterococ
Aba99669 Enterococ
AaK61368 Human imm
AaC16103 Human sec
Aac28915 Human sec
Aac02395 Human sec
Abn20425 Human ORF
Aba269409 Human COT
AaK79929 StephyLoc
AaI16353 Human imm
AaI6353 Prokaryot
Aac02463 Human sec
AaH33619 Human col
AaI12579 Human bla
Aac27012 Human sec
AaH82022 Rat diffe
Aba15216 Human pro
Aba166051 Lung can
Aba167339 Thyroid c
AaC12015 Human sec
AaH21976 Human adu

PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGETECH INC.
XX
PI Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR P-PSDB; AAB16529.
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Diaclosure; Page 157; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
XX
XX Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.6e-121;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTATTACGAATAGCGGAATCATACGCAAAATATTATCATGTTAAGGATTCGATTT 60
DB 1 ATGTATTACGAATAGCGGAATCATACGCAAAATATTATCATGTTAAGGATTCGATTT 60
QY 61 AAGCTATTCATTTTAAAGGTCATATGGCATATCATACAGTTAAAGATATGAACAC 120
DB 61 AAGCTATTCATTTTAAAGGTCATATGGCATATCATACAGTTAAAGATATGAACAC 120
QY 121 GTACCAATTAAACATGCTATATGTCATAGATGAGATGACTTATGTCAGCTTA 180
DB 121 GTACCAATTAAACATGCTATATGTCATAGATGAGATGACTTATGTCAGCTTA 180
QY 181 TTAAACCAAGCATAGATGATGATGAGAACACAGACGACAGACAGCTAAT 240
DB 181 TTAAACCAAGCATAGATGATGATGAGAACACAGACGACAGACAGCTAAT 240
QY 241 AACTAGTCATGAATGCTAG 261
DB 241 AACTAGTCATGAATGCTAG 261

RESULT 2
AAB68253

ID AAB68253 standard; DNA; 297 BP.
XX
XX AAB68253;
AC
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX Bacteriophage 77 77ORF182 nucleotide sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
XX *Staphylococcus aureus*; bacteriophage 77.
XX
XX WO200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
PF
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR P-PSDB; AAB16528.
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Diaclosure; Page 165; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
XX
XX Sequence 297 BP; 123 A; 40 C; 57 G; 77 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 261; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.6e-121;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTATTACGAATAAGCGAATCATACGCAAAAATATCATGTTAAGGATTCGATTTT 60
DB 37 ATGTATTACGAATAAGCGAATCATACGCAAAAATATTCATGTTAAGGATTCGATTTT 96
QY 61 AAGCTATTCATTTTAAAGGTCATATGGGCATTCATACATCAATGTTAAAGATAGAACAC 120
DB 97 AAGCTATTCATTTTAAAGGTCATATGGGCATTCATACATCAATGTTAAAGATAGAACAC 156
QY 121 GTACCAATTAACATGCTTATGTCGTAGATGAGATGACTTATGATGATGGCATCAAGCTTA 180
DB 137 GTACCAATTAACATGCTTATGTCGTAGATGAGATGACTTATGATGATGGCATCAAGCTTA 216
QY 181 TTTAACCAAGCATATGATGATGATTTGAAGAGACACAGACAGACAGACAGACTTAAT 240
DB 217 TTTAACCAAGCATATGATGATGATTTGAAGAGACACAGACAGACAGACAGACTTAAT 276
QY 241 AACTTAGTCATGAATGGTAG 261
DB 277 AACTTAGTCATGAATGGTAG 297

RESULT 3
AAA68247
ID AAA68247 standard; DNA; 41708 BP.
XX AAA68247;
AC
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX
DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
XX bacterial growth inhibition; bacterial infection; de.
OS *Staphylococcus aureus*; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1998; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGE TECH INC.
XX
XX
PI Pelletier J, Gros P, Dubow M;
XX

DR WPI; 2000-412361/35.
XX
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX
PS Example 3; Page 141-151; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (updated on 06-AUG-2003 to correct 05 field.)
CC (updated on 15-SEP-2003 to standardise 05 field)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 261; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2.9e-121;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTATTACGAATAAGCGAATCATACGCAAAAATATTCATGTTAAGGATTCGATTTT 60
DB 29304 ATGTATTACGAATAAGCGAATCATACGCAAAAATATTCATGTTAAGGATTCGATTTT 29363
QY 61 AAGCTATTCATTTTAAAGGTCATATGGGCATTCATACATCAATGTTAAAGATAGAACAC 120
DB 29364 AAGCTATTCATTTTAAAGGTCATATGGGCATTCATACATCAATGTTAAAGATAGAACAC 29423
QY 121 GTACCAATTAACATGCTTATGTCGTAGATGAGATGACTTATGATGATGGCATCAAGCTTA 180
DB 29424 GTACCAATTAACATGCTTATGTCGTAGATGAGATGACTTATGATGATGGCATCAAGCTTA 29483
QY 181 TTTAACCAAGCATATGATGATGATTTGAAGAGACACAGACAGACAGACAGACTTAAT 240
DB 29484 TTTAACCAAGCATATGATGATGATTTGAAGAGACACAGACAGACAGACAGACTTAAT 29543
QY 241 AACTTAGTCATGAATGGTAG 261
DB 29544 AACTTAGTCATGAATGGTAG 29564

RESULT 4
AAC86106
ID AAC86106 standard; cDNA; 41708 BP.
XX AAC86106;
XX
AC
XX
DT 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
XX Complete genome of bacteriophage 77.
DE

XX DnaI; *S. aureus*; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX Bacteriophage.
 OS
 XX WO200146383-A2.
 PN
 XX 28-JUN-2001.
 PD
 XX 21-DEC-2000; 2000WO-US035180.
 PF
 XX 22-DEC-1999; 99US-00470312.
 PR 12-OCT-2000; 2000US-00689952.
 XX
 XX (PHAG-) PHAGETECH INC.
 PA (WILL/) WILLIAMS K M.
 XX
 PI Pollettler J, Groe P, Dubow M;
 XX
 DR WPI; 2001-418052/44.
 XX
 XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by *Staphylococcus*
 PT *aureus*.
 XX
 XX Diacloaure; Flg 2; 107pp; English.
 XX
 CC This sequence represents the genome of Bacteriophage 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
 CC *aureus*, to form the basis of a screening assay. DnaI polypeptides and
 CC polynucleotides are useful for treating microbial, preferably bacterial,
 CC especially *Staphylococcus*, infections. DnaI polypeptides and
 CC polynucleotides are useful for biological, diagnostic, prophylactic,
 CC clinical and therapeutic use, and as components in databases useful for
 CC search analyses as well as in sequence analysis algorithms. (Updated on
 CC 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 261; DB 4; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 2.9e-121;
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTATTACGAATAGCGAAATCATACGCAAAATATTCTGTTACGATTCGATTTT 60
 DB 29304 ATGTATTACGAATAGCGAAATCATACGCAAAATATTCTGTTACGATTCGATTTT 29363
 QY 61 AAGCTATTCAATTTTAAAGGTCAATATGGGCATTCATACAGTATTAAGATATGAACAAC 120
 DB 29364 AAGCTATTCAATTTTAAAGGTCAATATGGGCATTCATACAGTATTAAGATATGAACAAC 29423
 QY 121 GTACCAATTAAACATGCTTATGTCGTAGATGAAGATGACTAGATATGGCATCAAGCTTA 180
 DB 29424 GTACCAATTAAACATGCTTATGTCGTAGATGAAGATGACTAGATATGGCATCAAGCTTA 29483
 QY 181 TTTAACCAAGCATAGATGATGATTGAAGAGAACACAGACAGACGACATGATTAAT 240

DB 29484 TTTAACCAAGCATAGATGATGATTGAAGAGAACACAGACAGACGACATGATTAAT 29543
 QY 241 AACTAGTCATGAATGGTAG 261
 DB 29544 AACTAGTCATGAATGGTAG 29564

RESULT 5
 ACF72925
 ID ACF72925 standard; DNA; 267 BP.
 XX
 AC ACF72925;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE *Staphylococcus aureus* DNA #605.
 XX
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target; gene; ds.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO200294868-A2.
 PD 28-NOV-2002.
 XX
 PF 27-MAR-2002; 2002WO-18002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Masignani V, More M, Scarselli M;
 XX
 DR WPI; 2003-120786/11.
 DR P-PSDB; ABM71365.
 XX
 PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing *Staphylococcus* infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 XX
 PS Claim 6; SEQ ID NO 1209; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus* bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* genes of the invention
 XX
 SQ Sequence 267 BP; 108 A; 31 C; 52 G; 76 T; 0 U; 0 Other;

CC	S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC	Including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC	skin and surgical wound infections, scalded skin syndrome, toxic shock
CC	syndrome, etc. Organisms transformed with the DNA sequences can be used
CC	for recombinant production of the polypeptides. The new DNA sequences
CC	(and their fragments) are useful as primers or probes for isolating
CC	homologues of any of the S.aureus DNA sequences contained on the computer
XX	readable medium
XQ	Sequence 580 BP; 255 A; 62 C; 123 G; 135 T; 0 U; 5 Other;
QY	Query Match 10.7%; Score 28; DB 2; Length 580;
Db	Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	234 ACTAATTAAGTTCGTCGAATGGTAG 261
Db	437 ACTAATTAAGTTCGTCGAATGGTAG 464
RESULT 7	
AAA68609	
ID	AAA68609 standard; DNA; 43576 BP.
AC	AAA68609;
XX	
DT	15-SEP-2003 (revised)
DT	06-AUG-2003 (revised)
DT	27-OCT-2000 (first entry)
DE	Bacteriophage 96 complete genome sequence.
XX	
KW	Bacteriophage; antimicrobial; genome; identification; antibacterial;
KM	bacterial growth inhibition; bacterial infection; ds.
OS	Staphylococcus aureus; bacteriophage 96.
PN	WO200032825-A2.
PD	08-JUN-2000.
PF	03-DEC-1999; 99WC-IB002040.
PR	03-DEC-1998; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407804.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168777P.
PR	02-DEC-1999; 99US-00454252.
PA	(PHAG-) PHAGETECH INC.
PI	Pelletier J, Gros P, Dubow M;
WPt	2000-412361/35.
Identifying a bacteriophage coding region for treating bacterial	

PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 PS Disclosure/ Page 190-198/ 456pp/ English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterized bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AA66243 to AA69442 and AA816323 to AA816934 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
 CC (Updated on 15-SEP-2003 to standardise 05 field)
 XX
 SQ Sequence 43576 BP; 16057 A; 6485 C; 8769 G; 12265 T; 0 U; 0 Other;
 Query Match 10.7%; Score 28; DB 3; Length 43576;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 234 ACTAATTAAGTTCATGCAATGGTAG 261
 DB 5235 ACTAATTAAGTTCATGCAATGGTAG 5262
 RESULT 8
 ACF73076
 ID ACF73076 standard; DNA; 258 BP.
 XX
 AC ACF73076;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus DNA #756.
 XX
 KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target; gene; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN W0200294868-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 27-MAR-2002; 2002WO-1B002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Maignani V, Mora M, Scarselli M;
 XX WPI; 2003-120786/11.
 DR P-PsDB; ABM71516.
 DR

XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX
 PS Claim 6; SEQ ID NO 1511; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus genes of the invention
 XX
 SQ Sequence 258 BP; 103 A; 31 C; 51 G; 73 T; 0 U; 0 Other;
 Query Match 9.6%; Score 25; DB 7; Length 258;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 234 ACTAATTAAGTTCATGCAATGG 258
 DB 234 ACTAATTAAGTTCATGCAATGG 258
 Search completed: October 15, 2004, 00:16:29
 Job time : 212.116 secs

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 22:42:59 ; Search time 1219.86 Seconds
(without alignments)
6389.277 Million cell updates/sec

SUMMARIES

28: gb_gss1:.*
29: gb_gss2:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

File:	US-09-407-804A-6	
Perfect score:	261	
Sequence:	1 atgtattacgaatagcgga.....actagtcataatgagtag 261	
Scoring table:	OLIGO_NUC Gapop 60.0 , Gapext 60.0	
Searched:	27513289 seqs, 14931090276 residues	
Word size :	0	
Total number of hits satisfying chosen parameters:	55026578	
Minimum DB seq length: 0		
Maximum DB seq length: 2000000000		
Post-processing: Listing first 1000 summaries		
Database :	EST:*	
	1:	em_ostba:*
	2:	em_osthu:*
	3:	em_ostln:*
	4:	em_ostnu:*
	5:	em_ostov:*
	6:	em_ostpl:*
	7:	em_ostro:*
	8:	em_hic:*
	9:	gb_ost1:*
	10:	gb_ost2:*
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	13:	gb_ost4:*
	14:	gb_ost5:*
	15:	em_ostfun:*
	16:	em_ostom:*
	17:	em_gss_hum:*
	18:	em_gss_inv:*
	19:	em_gss_pln:*
	20:	em_gss_vrt:*
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	22:	em_gss_mem:*
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	27:	em_gss_vrt:*

1	23	8.8	1015	29	CNS07DMP	AL440663 T3 end of
2	20	7.7	571	12	B0618748	B0618748 B0618748
3	20	7.7	736	28	BH514116	BH514116 BOHMB627E
4	19	7.3	121	9	A1951540	BH514116 BOHMB627E
5	19	7.3	423	28	BZ920613	A1951540 wv36407.*
6	19	7.3	522	29	CC428882	BZ920613 CH240_700
7	19	7.3	540	29	BK183031	CC428882 ZWMBE0242
8	19	7.3	614	28	AZ938354	BK183031 Danilo ferri
9	19	7.3	656	14	CB330526	AZ938354 ZM01964H21
10	19	7.3	663	29	CE786696	CB330526 SPEST506E
11	19	7.3	668	28	AZ466117	CE786696 tigr-gas-
12	19	7.3	672	28	AZ647829	AZ466117 IM0276N03-
13	19	7.3	686	28	AQ484294	AZ647829 IM0514J003
14	19	7.3	692	13	BK777633	AQ484294 RPCI-11-4
15	19	7.3	692	14	CA346528	BK777633 BX777633
16	19	7.3	738	13	BU492454	CA346528 677448 NC8
17	19	7.3	828	28	BZ422617	BU492454 604128953
18	19	7.3	923	28	AZ539374	BZ422617 tdsb06.b
19	19	7.3	935	28	AZ549644	AZ539374 ENTGH84TTE
20	19	7.3	937	28	BH165826	AZ549644 ENTEL62TTE
21	19	7.3	968	29	CC976887	BH165826 ENTQV67TTE
22	19	7.3	1349	10	BE973749	CC976887 ZUHA432TTE
23	18	6.9	303	28	AF179090	BE973749 60224781E
24	18	6.9	320	9	AA872489	AF179090 AF179090
25	18	6.9	347	29	CC859605	AA872489 o110c03.s
26	18	6.9	349	28	BH825920	CC859605 NDL_101N15
27	18	6.9	354	9	AA282587	BH825920 BACP22-20
28	18	6.9	360	28	AQ265943	AA282587 z90c02.r
29	18	6.9	390	28	B37409	AQ265943 CTIPI-E1
30	18	6.9	405	29	CE641065	B37409 HS-1043-B1
31	18	6.9	408	9	AA088591	CE641065 tigr-gas-
32	18	6.9	409	9	AA630685	AA088591 zK64d07.r
33	18	6.9	412	9	AA255702	AA630685 ae63h06.s
34	18	6.9	414	10	AM917645	AA255702 z921c04.r
35	18	6.9	414	13	BY484641	AM917645 EST34894470
36	18	6.9	416	28	AZ598867	BY484641 BY484641
37	18	6.9	420	10	AM917612	AZ598867 IM0413H227
38	18	6.9	420	10	AM917643	AM917612 EST34891G
39	18	6.9	444	28	BH212049	AM917643 EST3489470
40	18	6.9	457	29	CE704213	BH212049 SALK_007070
41	18	6.9	458	9	AA047153	CE704213 tigr-gas-
42	18	6.9	461	12	BJ046548	AA047153 zK74f07.r
43	18	6.9	462	13	BY573081	BJ046548 BJ046548
44	18	6.9	463	29	CG985891	BY573081 BY573081
45	18	6.9	468	14	T89328	CG985891 CH240_156E
						T89328 v013909.s1

c	46	18	6.9	486	29	BK124558	BK124558	Datlo	ref	c	103	18	6.9	717	29	CG275417	CG275417	OGKCT06TH	
c	47	18	6.9	494	12	B046014	B046014			c	104	18	6.9	720	29	QNS00WG	AL093910	ArbIdcdops	
c	48	18	6.9	495	13	BK872646	BK872646			c	105	18	6.9	723	28	B2458710	B2458710	ArbIdcdops	
c	49	18	6.9	508	28	AQ375859	AQ375859	RPCT11-14		c	106	18	6.9	725	9	A1290974	A1290974	GM15C08.x	
c	50	18	6.9	509	9	AW021842	AW021842	dft29a06.y		c	107	18	6.9	748	12	B1087876	B1087876	602852679	
c	51	18	6.9	510	12	B1963093	B1963093	1a65906.y		c	108	18	6.9	760	14	CA312676	CA312676	UT-CF-FNO	
c	52	18	6.9	511	9	AA801416	AA801416	EST190913		c	109	18	6.9	779	10	BES39851	BES39851	601061965	
c	53	18	6.9	511	9	AA146650	AA146650	z043d12.r		c	110	18	6.9	780	28	B2085908	B2085908	11h3b01.	
c	54	18	6.9	515	10	BE033138	BE033138	133469 MA		c	111	18	6.9	785	13	BU246775	BU246775	603593512	
c	55	18	6.9	518	9	A1958218	A1958218	fc92d12.y		c	112	18	6.9	790	28	BH527597	BH527597	BOGZEF30TR	
c	56	18	6.9	524	12	BJ642732	BJ642732	BJ642732		c	113	18	6.9	799	29	BX200998	BX200998	Datlo	ref
c	57	18	6.9	532	14	CB718807	CB718807	AMGNMNC.N		c	114	18	6.9	804	13	BE620191	BE620191	UT-H-FIL-	
c	58	18	6.9	532	29	CE201002	CE201002	ti9f-9ss-		c	115	18	6.9	811	10	BE614108	BE614108	601503850	
c	59	18	6.9	533	28	AZ535820	AZ535820	RPCT-23-1		c	116	18	6.9	824	9	AU118315	AU118315	AO118315	
c	60	18	6.9	533	28	BZ518982	BZ518982	BOWP21.6TR		c	117	18	6.9	830	12	BG784002	BG784002	SEAMC003	
c	61	18	6.9	546	13	BU395921	BU395921	603802505		c	118	18	6.9	833	28	AZ702636	AZ702636	RPCT-23-2	
c	62	18	6.9	547	10	BF549762	BF549762	UI-R-AO-a		c	119	18	6.9	838	28	BH660714	BH660714	BOWFM1.2TR	
c	63	18	6.9	563	9	AV590721	AV590721	AV590721		c	120	18	6.9	841	13	BU116745	BU116745	SOY139747	
c	64	18	6.9	563	12	BM190058	BM190058	POSM01.000		c	121	18	6.9	843	29	CG825123	CG825123	SOY139747	
c	65	18	6.9	564	28	BH008399	BH008399	q135c01.x		c	122	18	6.9	846	14	CA987036	CA987036	AGENC00RT	
c	66	18	6.9	573	12	BI444760	BI444760	daa93a07.		c	123	18	6.9	847	10	BF694081	BF694081	602082686	
c	67	18	6.9	575	29	CE495919	CE495919	ti9f-9ss-		c	124	18	6.9	855	13	BK467886	BK467886	602441871	
c	68	18	6.9	578	14	CA386811	CA386811	668508 NC		c	125	18	6.9	872	12	BG399577	BG399577	602441871	
c	69	18	6.9	584	14	CD678706	CD678706	hpl2b06.y		c	126	18	6.9	891	10	BF618320	BF618320	HYSMC000	
c	70	18	6.9	588	14	CA650925	CA650925	wrcin.pk1		c	127	18	6.9	900	29	CC509879	CC509879	CH240..353	
c	71	18	6.9	590	9	AL704631	AL704631	DKF26680		c	128	18	6.9	910	13	BU201993	BU201993	603951810	
c	72	18	6.9	592	9	AA818734	AA818734	UI-R-AO-a		c	129	18	6.9	920	14	CF108627	CF108627	Shu1tzcml	
c	73	18	6.9	598	12	BM970383	BM970383	UI-CF-ECL		c	130	18	6.9	937	13	BU481226	BU481226	60466859	
c	74	18	6.9	602	13	BU070239	BU070239	1m11b01.x		c	131	18	6.9	964	10	BF209546	BF209546	601872730	
c	75	18	6.9	606	9	AA149491	AA149491	z128b03..r		c	132	18	6.9	998	28	B2466016	B2466016	BONK647F	
c	76	18	6.9	606	14	CA375660	CA375660	653788 NC		c	133	18	6.9	1149	28	CC274398	CC274398	CH261-112	
c	77	18	6.9	609	14	CD931537	CD931537	GR45.114M		c	134	18	6.9	1183	10	BE875365	BE875365	601487003	
c	78	18	6.9	628	12	BM509287	BM509287	1h.19h05.x		c	135	18	6.9	4693	11	AK081376	AK081376	Mus mmscu	
c	79	18	6.9	632	12	BI492771	BI492771	dft29a06.w		c	136	18	6.9	178	14	CB870415	CB870415	cta0b0m0	
c	80	18	6.9	645	29	CE511088	CE511088	ti9f-9ss-		c	137	18	6.9	190	14	CB485548	CB485548	ctb0b0m0	
c	81	18	6.9	648	12	BJ091083	BJ091083	603258238		c	138	18	6.9	212	10	BF228723	BF228723	SMVYJ3CAN	
c	82	18	6.9	650	14	CA780127	CA780127	MPJ384.4		c	139	18	6.9	227	13	BE009943	BE009943	PMS-BN017	
c	83	18	6.9	653	28	AZ638156	AZ638156	1m0497120		c	140	18	6.9	227	13	BQ537041	BQ537041	PFTST0ab2	
c	84	18	6.9	656	29	CG069104	CG069104	FUIMM41TD		c	141	18	6.9	229	12	BM027341	BM027341	G1T000068	
c	85	18	6.9	657	13	BU433855	BU433855	603258238		c	142	18	6.9	233	28	AZ782938	AZ782938	2M0024P12	
c	86	18	6.9	667	10	BE535553	BE535553	601060265		c	143	18	6.9	243	9	AU059887	AU059887	AU059887	
c	87	18	6.9	672	14	CA310990	CA310990	UI-CF-FNO		c	144	18	6.9	245	9	AL715175	AL715175	AL715175	
c	88	18	6.9	677	13	BQ477501	BQ477501	1k87g12.x		c	145	18	6.9	247	9	AA121205	AA121205	zn30b10..f	
c	89	18	6.9	681	12	BM491033	BM491033	p9g2n.pk0		c	146	18	6.9	260	13	BQ757813	BQ757813	EBem10..SQ	
c	90	18	6.9	682	28	BH425060	BH425060	BOHNU11TR		c	147	18	6.9	263	14	CD141160	CD141160	MGI-0069T	
c	91	18	6.9	682	29	CE721090	CE721090	ti9f-9ss-		c	148	18	6.9	282	10	BF803200	BF803200	CNO-CI013	
c	92	18	6.9	685	14	CD931536	CD931536	GR45.114M		c	149	18	6.9	287	12	BI703410	BI703410	f890c04..x	
c	93	18	6.9	688	14	CA367832	CA367832	643832 NC		c	150	18	6.9	298	9	AV339528	AV339528	AV339528	
c	94	18	6.9	688	14	CA775922	CA775922	1p01g11.x		c	151	18	6.9	299	14	CD063005	CD063005	MAL-0029U	
c	95	18	6.9	698	28	AZ702634	AZ702634	RPCT-23-2		c	152	18	6.9	301	9	AV428985	AV428985	AV428985	
c	96	18	6.9	699	14	CB466979	CB466979	732693 MA		c	153	18	6.9	305	12	BI703411	BI703411	f890c04..y	
c	97	18	6.9	705	14	CF795789	CF795789	891982 MA		c	154	18	6.9	314	14	CF002778	CF002778	QBH1506..	
c	98	18	6.9	706	13	BK488598	BK488598	DKF2P686L		c	155	18	6.9	321	14	CD159773	CD159773	MAL-0064G	
c	99	18	6.9	708	12	BG809404	BG809404	mghe0032x		c	156	18	6.9	325	12	BG354250	BG354250	941033D10	
c	100	18	6.9	710	13	BU677557	BU677557	UI-CF-EEO		c	157	18	6.9	338	12	BI350479	BI350479	f890c04..x	
c	101	18	6.9	713	29	BK172652	BK172652	Datlo	ref	c	158	18	6.9	340	9	AL501134	AL501134	AL501134	
c	102	18	6.9	715	29	CE217017	CE217017	ti9f-9ss-		c	159	18	6.9	345	10	AW481192	AW481192	34786 MAR	

c 160	17	6.5	347	13	CA000609	217	17	6.5	463	14	CF165371
c 161	17	6.5	348	9	AA487238	c 218	17	6.5	463	28	AZ445372
c 162	17	6.5	351	28	AZ417905	219	17	6.5	466	28	AZ647024
c 163	17	6.5	352	13	BQ518498	220	17	6.5	476	14	CD153135
c 164	17	6.5	359	29	CE018865	221	17	6.5	479	28	AZ165551
c 165	17	6.5	360	13	CA7083	222	17	6.5	485	29	CE629783
c 166	17	6.5	360	14	D76260	c 223	17	6.5	486	28	BH437009
c 167	17	6.5	360	28	CC428366	c 224	17	6.5	490	14	CD923032
c 168	17	6.5	361	10	AV164055	c 225	17	6.5	490	28	AQ213527
c 169	17	6.5	361	12	BI703322	c 226	17	6.5	495	9	AA534580
c 170	17	6.5	364	28	AZ702724	c 227	17	6.5	495	12	BM737776
c 171	17	6.5	365	12	BG380121	c 228	17	6.5	496	12	BM737776
c 172	17	6.5	378	14	CD171473	c 229	17	6.5	496	12	BM737776
c 173	17	6.5	382	12	BI863990	c 230	17	6.5	498	12	BM959014
c 174	17	6.5	386	13	BH882152	c 231	17	6.5	500	9	AU086596
c 175	17	6.5	388	12	BI992287	c 232	17	6.5	501	12	BJ462291
c 176	17	6.5	394	13	BK492477	c 233	17	6.5	503	29	CG161066
c 177	17	6.5	395	13	BY615376	c 234	17	6.5	504	10	BF439218
c 178	17	6.5	399	9	AV653367	c 235	17	6.5	510	28	AQ440696
c 179	17	6.5	399	9	AV653455	c 236	17	6.5	513	29	CG865295
c 180	17	6.5	403	13	BY510745	c 237	17	6.5	516	10	BB640566
c 181	17	6.5	403	14	CB768715	c 238	17	6.5	516	10	BB640566
c 182	17	6.5	405	14	CD066383	c 239	17	6.5	518	9	AJ732799
c 183	17	6.5	407	9	AA332691	c 240	17	6.5	518	10	AM505521
c 184	17	6.5	408	10	BB237268	c 241	17	6.5	518	12	BM959057
c 185	17	6.5	410	28	AQ363028	c 242	17	6.5	518	12	BM959057
c 186	17	6.5	411	9	AV610147	c 243	17	6.5	518	14	CA360520
c 187	17	6.5	414	13	BY623508	c 244	17	6.5	519	13	CA000637
c 188	17	6.5	417	14	CD180546	c 245	17	6.5	520	12	BI864898
c 189	17	6.5	417	28	AQ186008	c 246	17	6.5	524	14	CD552921
c 190	17	6.5	419	9	AA487179	c 247	17	6.5	524	28	AZ433259
c 191	17	6.5	421	13	BQ662116	c 248	17	6.5	526	12	BI350855
c 192	17	6.5	423	29	CC945736	c 249	17	6.5	528	14	CB485130
c 193	17	6.5	424	14	BM179786	c 250	17	6.5	529	14	N65371
c 194	17	6.5	427	12	BM172861	c 251	17	6.5	532	13	CA001132
c 195	17	6.5	428	29	CE292254	c 252	17	6.5	533	28	BH774336
c 196	17	6.5	434	9	AV792912	c 253	17	6.5	533	28	AZ058253
c 197	17	6.5	436	14	CB792912	c 254	17	6.5	535	28	AQ582734
c 198	17	6.5	439	14	CD071932	c 255	17	6.5	536	14	CB223434
c 199	17	6.5	442	14	CD163698	c 256	17	6.5	536	28	B2130904
c 200	17	6.5	442	29	DR424167	c 257	17	6.5	537	28	AZ043135
c 201	17	6.5	443	10	BB736326	c 258	17	6.5	538	13	BY474795
c 202	17	6.5	443	10	BB840465	c 259	17	6.5	539	9	AL911728
c 203	17	6.5	443	28	AQ333975	c 260	17	6.5	539	12	AL925185
c 204	17	6.5	444	28	AZ664379	c 261	17	6.5	539	12	BJ019717
c 205	17	6.5	445	14	N65216	c 262	17	6.5	541	12	BG082063
c 206	17	6.5	446	14	CD159741	c 263	17	6.5	541	12	BM160508
c 207	17	6.5	447	13	BK556924	c 264	17	6.5	541	14	CF893896
c 208	17	6.5	449	9	A1384718	c 265	17	6.5	543	28	AZ521059
c 209	17	6.5	455	13	BY472564	c 266	17	6.5	544	28	AZ043949
c 210	17	6.5	455	14	H43732	c 267	17	6.5	546	10	AM333199
c 211	17	6.5	458	9	AJ283752	c 268	17	6.5	548	14	CA194954
c 212	17	6.5	459	9	AA794496	c 269	17	6.5	548	14	CE532854
c 213	17	6.5	460	14	CB737792	c 270	17	6.5	550	10	AM773600
c 214	17	6.5	460	14	CD159785	c 271	17	6.5	551	12	BI429315
c 215	17	6.5	462	12	BI880146	c 272	17	6.5	552	12	BI428471
c 216	17	6.5	462	29	CE697617						

c 273	17	6.5	553	28	AQ410320	AQ410320 HS_5111_A	330	17	6.5	605	28	AZ459386	AZ459386 1M0264L11
274	17	6.5	556	14	CDL85112	CDL85112 NS1-0051T	331	17	6.5	605	28	BZ709988	BZ709988 OCGA0037C
275	17	6.5	558	12	BI936043	BI936043 PFEStGa2	c 332	17	6.5	607	12	BI267928	BI267928 NF114H121
276	17	6.5	559	14	CB536735	CB536735 771778 NA	333	17	6.5	607	14	CB244577	CB244577 UI-M-FY0-
c 277	17	6.5	562	10	AW335125	AW335125 54381 AGS	c 334	17	6.5	607	29	CE723430	CE723430 t1gr-gss-
c 278	17	6.5	563	9	AU024507	AU024507 AU024507	335	17	6.5	611	12	EM072582	EM072582 fV08H05.Y
c 279	17	6.5	563	10	BE122231	BE122231 945039E01	c 336	17	6.5	611	28	AZ418660	AZ418660 1M0194014
c 280	17	6.5	563	28	AO922373	AO922373 RPECI-23-2	c 337	17	6.5	612	13	BK621393	BK621393 BX621393
c 281	17	6.5	563	28	BE759503	BE759503 621_4L_G1	c 338	17	6.5	615	28	BZ423878	BZ423878 1D54405.g
c 282	17	6.5	564	12	BK525530	BK525530 fK64B05.Y	c 339	17	6.5	618	28	AZ247021	AZ247021 RPECI-23-9
c 283	17	6.5	565	28	AQ720634	AQ720634 HS_5546_B	c 340	17	6.5	619	12	B1126743	B1126743 B1126743
284	17	6.5	566	29	CE095411	CE095411 t1gr-gss-	c 341	17	6.5	620	10	BE605965	BE605965 f124603.x
285	17	6.5	569	12	BM275708	BM275708 PFEStGa5	c 342	17	6.5	622	12	B0513713	B0513713 B0513713
c 286	17	6.5	569	13	BK737918	BK737918 BX737918	c 343	17	6.5	623	14	CB521333	CB521333 UI-M-GHO-
c 287	17	6.5	569	28	BE679198	BE679198 PUBB249TD	c 344	17	6.5	625	10	BF670958	BF670958 602150759
288	17	6.5	570	12	BK274525	BK274525 PFEStGa4	c 345	17	6.5	625	28	BH082279	BH082279 RPECI-24-3
c 289	17	6.5	571	12	BI841775	BI841775 f102B09.Y	c 346	17	6.5	626	10	BB650336	BB650336 BB650326
c 290	17	6.5	571	29	CE758952	CE758952 t1gr-gss-	c 347	17	6.5	626	28	B2106398	B2106398 CH230-204
c 291	17	6.5	572	12	BM879432	BM879432 Kt95a09.Y	c 348	17	6.5	628	12	BI475402	BI475402 fQ32B05.Y
c 292	17	6.5	574	12	B4544466	B4544466 BU454466	c 349	17	6.5	628	12	BM079729	BM079729 MESt98-G0
c 293	17	6.5	574	14	CF892995	CF892995 A0117E04-	c 350	17	6.5	628	28	AZ418043	AZ418043 UI-M-EXO-
c 294	17	6.5	575	13	BQ141374	BQ141374 NF01BH07P	c 351	17	6.5	629	14	CB249003	CB249003 UI-M-EXO-
c 295	17	6.5	576	13	BQ074286	BQ074286 f227A08.Y	c 352	17	6.5	631	28	AZ641567	AZ641567 1M0504X07
c 296	17	6.5	577	12	BI325517	BI325517 f139C02.X	c 353	17	6.5	632	10	BE413502	BE413502 MC0010.B0
c 297	17	6.5	577	12	BI533342	BI533342 f180F12.X	c 354	17	6.5	632	12	BM172610	BM172610 1Im9eqC-3
298	17	6.5	578	12	BM275410	BM275410 PFEStGa6	c 355	17	6.5	632	28	BH830418	BH830418 BACP31-B
299	17	6.5	578	29	CE098477	CE098477 t1gr-gss-	c 356	17	6.5	634	14	CB429663	CB429663 605496 NA
300	17	6.5	580	12	BM160962	BM160962 EST563485	c 357	17	6.5	635	28	AZ290863	AZ290863 RPECI-23-1
301	17	6.5	581	12	BG226353	BG226353 Kq20612.Y	c 358	17	6.5	636	12	BM958079	BM958079 fY13A09.X
c 302	17	6.5	582	12	BI311979	BI311979 EST531372	c 359	17	6.5	636	14	CF746138	CF746138 UI-M-GVO-
c 303	17	6.5	582	29	LABF046A01	LABF046A01 Le1ahmari	c 360	17	6.5	636	29	CE707246	CE707246 t1gr-gss-
c 304	17	6.5	583	12	B4448769	B4448769 BU448769	c 361	17	6.5	637	29	CG037889	CG037889 PUFMD06TB
305	17	6.5	583	13	BK627326	BK627326 BX627326	c 362	17	6.5	638	10	AM970281	AM970281 EST382362
306	17	6.5	586	12	BI429187	BI429187 f174B03.Y	c 363	17	6.5	640	13	CA056903	CA056903 s661rb52
307	17	6.5	587	12	BI982650	BI982650 f556c10.Y	c 364	17	6.5	640	13	CF743537	CF743537 UI-M-GIO-
c 308	17	6.5	587	28	AZ646858	AZ646858 2M0147A14	c 365	17	6.5	640	14	CB521158	CB521158 UI-M-GHO-
c 309	17	6.5	588	12	BM959194	BM959194 PLATE.17	c 366	17	6.5	641	28	BH025055	BH025055 RPECI-24-2
310	17	6.5	588	14	CB353383	CB353383 2F001-P00	c 367	17	6.5	641	28	BZ627272	BZ627272 1H51d09.b
311	17	6.5	588	14	CS519287	CS519287 UI-M-GHO-	c 368	17	6.5	642	12	BG873872	BG873872 MESt43-F0
c 312	17	6.5	590	10	AM281818	AM281818 f157d10.X	c 369	17	6.5	643	14	CF532744	CF532744 UI-M-GHO-
313	17	6.5	590	13	BQ180297	BQ180297 UI-M-EXO-	c 370	17	6.5	644	13	BK510120	BK510120 DKF2686D
314	17	6.5	592	12	BI429029	BI429029 f171e03.Y	c 371	17	6.5	644	14	CF745029	CF745029 UI-M-GVO-
c 315	17	6.5	597	28	CC939370	CC939370 PUBF1A3TD	c 372	17	6.5	646	14	CB723748	CB723748 UI-M-FY0-
316	17	6.5	598	12	B4497547	B4497547 BU497547	c 373	17	6.5	647	9	AU253519	AU253519 AU253519
317	17	6.5	598	13	BQ723941	BQ723941 AGENCCURT	c 374	17	6.5	652	13	CA160894	CA160894 SCACR2306
c 318	17	6.5	599	10	AM967905	AM967905 EST379980	c 375	17	6.5	655	29	AG148030	AG148030 Pan treq1
c 319	17	6.5	600	12	BG802981	BG802981 0193-45 M	c 376	17	6.5	656	28	AZ369500	AZ369500 1M0120D10
c 320	17	6.5	600	13	BU919815	BU919815 6041-11 M	c 377	17	6.5	657	12	B1509403	B1509403 B0509403
c 321	17	6.5	602	9	AL699109	AL699109 DKF2686B	c 378	17	6.5	657	13	BQ480954	BQ480954 f66724806.
c 322	17	6.5	602	9	AL719598	AL719598 AL719598	c 379	17	6.5	663	13	BU715011	BU715011 SUNBSP01
c 323	17	6.5	602	12	B0103294	B0103294 BU103294	c 380	17	6.5	663	14	CB519872	CB519872 UI-M-GHO-
c 324	17	6.5	602	13	BK082315	BK082315 BX082315	c 381	17	6.5	665	13	BY741953	BY741953 BU741953
c 325	17	6.5	602	13	CA025081	CA025081 H251C14f	c 382	17	6.5	666	14	CF540041	CF540041 UI-M-EXO-
c 326	17	6.5	602	29	CE203989	CE203989 t1gr-gss-	c 383	17	6.5	667	10	BB51610	BB51610 BB51610
c 327	17	6.5	603	13	AM970362	AM970362 EST382443	c 384	17	6.5	667	28	AZ245826	AZ245826 RPECI-23-4
328	17	6.5	604	13	BQ075080	BQ075080 f227A08.X	c 385	17	6.5	669	12	BI261287	BI261287 602969018
329	17	6.5	604	14	CF622008	CF622008 lat11908.	c 386	17	6.5	669	28	BH959056	BH959056 ocl08A04.

387	17	6.5	670	14	CD348458	CD348458	UI-M-FY0-	444	17	726	14	CF536851	CF536851	UI-M-FY0-
388	17	6.5	670	28	A20593842	A20593842	RPCT-23-4	445	17	726	28	BH007589	BH007589	e071c03.x
389	17	6.5	671	14	CF744025	CF744025	UI-M-GV0-	446	17	727	12	BG618564	BG618564	602645477
390	17	6.5	672	29	CS820908	CS820908	SOYAU8VTV	447	17	728	14	CD348418	CD348418	UI-M-FY0-
391	17	6.5	673	13	BK305022	BK305022	BX305022	448	17	729	11	CNS0803G	CNS0803G	Single fe
392	17	6.5	675	28	A2468744	A2468744	1M0281J17	449	17	730	13	BU378789	BU378789	604171355
393	17	6.5	676	9	AV653243	AV653243	AV653243	450	17	730	28	AQ291302	AQ291302	nbdb0038D
394	17	6.5	678	29	CG052463	CG052463	PUEM42TD	451	17	730	28	B2368356	B2368356	1d12h04.g
395	17	6.5	678	14	CB214436	CB214436	OMLO4716	452	17	731	29	CC504377	CC504377	CH240.344
396	17	6.5	682	28	CC324799	CC324799	TAM32-10C	453	17	732	12	BH943819	BH943819	UI-M-EHPD
397	17	6.5	683	28	BH824542	BH824542	BACP20-N	454	17	733	12	BM954892	BM954892	UI-M-FY0-
398	17	6.5	689	14	CS519117	CS519117	UI-M-GH0-	455	17	735	12	B1738892	B1738892	603362590
399	17	6.5	689	14	CS248922	CS248922	UI-M-EX0-	456	17	735	12	CB249760	CB249760	Pan treg1
400	17	6.5	690	14	CS249531	CS249531	UI-M-EX0-	457	17	736	29	AG081460	AG081460	UI-M-EX0-
401	17	6.5	690	14	CS447711	CS447711	701732 MA	458	17	738	14	CS520841	CS520841	UI-M-GH0-
402	17	6.5	694	14	CS525130	CS525130	UI-M-FY0-	459	17	741	13	BQ180496	BQ180496	UI-M-EX0-
403	17	6.5	695	14	CB249774	CB249774	UI-M-EX0-	460	17	741	13	CA139810	CA139810	SC2ZFR201
404	17	6.5	695	29	CC711044	CC711044	OG0ED34TV	461	17	742	14	CB519090	CB519090	UI-M-GH0-
405	17	6.5	696	28	B2423864	B2423864	1d5c02.g	462	17	743	13	BX081851	BX081851	BX081851
406	17	6.5	698	14	CM233312	CM233312	AGENCOURT	463	17	743	14	CA752208	CA752208	UI-M-FY0-
407	17	6.5	699	13	BU722530	BU722530	SCMAJC03	464	17	744	13	CF182743	CF182743	UI-M-EY0-
408	17	6.5	700	12	BP115175	BP115175	BP115175	465	17	747	14	CC128652	CC128652	NID1-4C13.
409	17	6.5	700	14	CD578408	CD578408	UI-M-FY0-	466	17	748	28	CC247469	CC247469	CH261-15E
410	17	6.5	701	13	BK673897	BK673897	RPCT-24-2	467	17	752	14	CB521168	CB521168	UI-M-GH0-
411	17	6.5	701	28	BH054777	BH054777	663680 NC	468	17	753	14	CA318569	CA318569	UI-M-FY0-
412	17	6.5	702	14	CA388914	CA388914	CSU-K33.r	469	17	753	14	BM167220	BM167220	ES75.69743
413	17	6.5	702	28	CC072258	CC072258	MBEKB55TF	470	17	754	12	CS519577	CS519577	UI-M-GH0-
414	17	6.5	704	29	CS924814	CS924814	601659850	471	17	754	14	CB519577	CB519577	UI-M-GH0-
415	17	6.5	707	10	BE965957	BE965957	601659850	472	17	755	14	CF532371	CF532371	UI-M-GH0-
416	17	6.5	707	14	CS528208	CS528208	PMO-NN004	473	17	755	13	BX082316	BX082316	BX082316
417	17	6.5	708	10	BF362333	BF362333	BU508392	474	17	758	13	BX081852	BX081852	BX081852
418	17	6.5	708	12	BU508392	BU508392	UI-M-EX0-	475	17	760	28	B2709997	B2709997	OGDA0037M
419	17	6.5	708	13	BQ442269	BQ442269	UI-M-EX0-	476	17	761	13	BX082712	BX082712	MBEJY72TR
420	17	6.5	709	14	CF728091	CF728091	UI-M-GH0-	477	17	762	12	BM963405	BM963405	UI-M-EY0-
421	17	6.5	709	14	CF534097	CF534097	UI-M-EX0-	478	17	763	12	BU533156	BU533156	BJ533156
422	17	6.5	710	13	BO180624	BO180624	UI-M-EX0-	479	17	763	14	CM027696	CM027696	AGENCOURT
423	17	6.5	711	12	BJ021333	BJ021333	UI-M-EX0-	480	17	764	29	CG761621	CG761621	ZMMBB033
424	17	6.5	711	13	BK077221	BK077221	H3072A10-	481	17	764	29	CG888560	CG888560	ZMMBB036
425	17	6.5	712	10	BG069039	BG069039	ZMMBB015	482	17	765	13	BU611625	BU611625	UI-M-FY0-
426	17	6.5	712	29	CC790062	CC790062	BM963405	483	17	766	29	CG952252	CG952252	MBEJY72TR
427	17	6.5	712	29	CS693958	CS693958	BM963405	484	17	774	14	CF535686	CF535686	UI-M-GH0-
428	17	6.5	713	12	BU540962	BU540962	UI-M-FY0-	485	17	775	29	CG904137	CG904137	ZMMBB051
429	17	6.5	713	14	CA325245	CA325245	UI-M-FY0-	486	17	777	14	CF182550	CF182550	UI-M-EY0-
430	17	6.5	713	14	CF182447	CF182447	UI-M-EY0-	487	17	782	29	CNS01KVM	CNS01KVM	ANCPHEL9s
431	17	6.5	713	29	CS338908	CS338908	UI-M-FY0-	488	17	784	13	BX083167	BX083167	BX083167
432	17	6.5	714	14	CF534147	CF534147	UI-M-GH0-	489	17	785	12	B1851873	B1851873	603378030
433	17	6.5	717	13	BO546146	BO546146	EST629773	490	17	785	13	BX073840	BX073840	BM963405
434	17	6.5	717	14	CB249979	CB249979	UI-M-EX0-	491	17	785	13	BU238786	BU238786	603322479
435	17	6.5	717	14	CS526633	CS526633	UI-M-FY0-	492	17	796	14	CF550433	CF550433	AGENCOURT
436	17	6.5	717	28	A2381379	A2381379	1M0137K24	493	17	801	28	BH069243	BH069243	RPCT-24-2
437	17	6.5	720	12	BU539515	BU539515	665776 NC	494	17	807	13	BK077222	BK077222	CG1X06422
438	17	6.5	722	14	CA388982	CA388982	UI-M-EX0-	495	17	808	14	CA969404	CA969404	CH240.419
439	17	6.5	723	14	CB248828	CB248828	UI-M-FY0-	496	17	809	29	CC539302	CC539302	ZMMBB030
440	17	6.5	723	14	CB289996	CB289996	UI-M-FY0-	497	17	816	28	CC173934	CC173934	AGENCOURT
441	17	6.5	723	29	CF761977	CF761977	t1qf-gas-	498	17	818	14	CM027506	CM027506	ZMMBB030
442	17	6.5	724	14	CB429306	CB429306	603113 MA	499	17	823	12	B1852870	B1852870	603379161
443	17	6.5	726	14	CA919348	CA919348	EST637066	500	17	831	28	B2463862	B2463862	BONR026TF

501	17	6.5	831	28	B2604705	WHAB1207R	558	17	6.5	1299	29	CG750474	CG750474 P045-1-B0
502	17	6.5	832	13	B0958973	AGENCOURT	c 559	17	6.5	1315	29	CG749195	CG749195 P043-2-D0
503	17	6.5	832	14	C0652343	AGENCOURT	c 560	17	6.5	1320	29	CG755797	CG755797 P051-2-B0
504	17	6.5	837	13	BK078183	BK078183	c 561	17	6.5	1326	11	AY109265	AY109265 Zeeb maya
505	17	6.5	843	29	CG922445	MBEMF84TF	562	17	6.5	1360	29	CG757149	CG757149 P052-2-D0
506	17	6.5	844	14	CF662055	CCLX13A40	563	17	6.5	1370	29	CG757666	CG757666 P053-1-B0
507	17	6.5	847	13	BK082517	BK082517	564	17	6.5	1385	29	CG757667	CG757667 P053-1-B0
508	17	6.5	847	29	CC538494	CC538494	c 565	17	6.5	1812	28	B2572834	B2572834 msh2_2822
509	17	6.5	861	13	B091896	B091896	566	17	6.5	2914	11	AK044809	AK044809 Mus muscu
510	17	6.5	861	28	A2197691	SP_1035_B	567	17	6.5	3404	11	AK046376	AK046376 Mus muscu
511	17	6.5	867	29	CNS04E1H	AL287090 Tetraodon	568	17	6.5	4793	11	AK049003	AK049003 Mus muscu
512	17	6.5	868	14	CBS14443	CBS14443	569	17	6.5	7886	11	BC034956	BC034956 Homo sapi
513	17	6.5	873	13	BQ229068	BQ229068	570	17	6.5	113	10	AM493141	AM493141 UI-M-BH3-
514	17	6.5	875	13	BK083032	BK083032	571	17	6.5	128	28	A2121241	A2121241 RPCT-23-1
515	17	6.5	877	13	BQ716790	BQ716790	c 572	17	6.5	131	12	BG125723	BG125723 EST471369
516	17	6.5	883	28	B2411388	B2411388	573	17	6.5	139	9	AV331698	AV331698 AV331698
517	17	6.5	889	14	CBS11722	CBS11722	574	17	6.5	144	10	BM373750	BM373750 BM373750
518	17	6.5	896	13	B0908189	B0908189	575	17	6.5	146	12	BM385843	BM385843 UI-R-DH1-
519	17	6.5	903	29	CG955735	CG955735	c 576	17	6.5	146	12	BM196797	BM196797 C0337F11-
520	17	6.5	904	28	A2538065	A2538065	577	17	6.5	157	28	CC152863	CC152863 CSU-K34.1
521	17	6.5	904	28	B2176853	B2176853	c 578	17	6.5	158	10	BB278128	BB278128 BB278128
522	17	6.5	915	10	BF739615	BF739615	c 579	17	6.5	165	13	BY373743	BY373743 BY373743
523	17	6.5	921	10	BF689582	BF689582	c 580	17	6.5	166	13	BY461142	BY461142 BY461142
524	17	6.5	924	29	CNS04DEL	AL285654 Tetraodon	581	17	6.5	167	10	BB860644	BB860644 UI-M-AH1-
525	17	6.5	926	29	AG131045	AG131045	c 582	17	6.5	170	10	BB849050	BB849050 UI-M-AH1-
526	17	6.5	932	10	BF794648	BF794648	c 583	17	6.5	174	12	BM974993	BM974993 UI-CF-EC1
527	17	6.5	938	10	BB896784	BB896784	584	17	6.5	177	9	A1795260	A1795260 RRACA961
528	17	6.5	944	10	BF104206	BF104206	c 585	17	6.5	190	10	BB569076	BB569076 RRACA961
529	17	6.5	944	28	A2166857	A2166857	c 586	17	6.5	191	9	A1566420	A1566420 t99c09.x
530	17	6.5	945	29	CG187851	CG187851	c 587	17	6.5	194	14	H31987	H31987
531	17	6.5	953	28	A2546793	A2546793	588	17	6.5	198	29	CE341223	CE341223 t19t-gss-
532	17	6.5	962	29	CG864763	CG864763	589	17	6.5	199	10	BB526321	BB526321
533	17	6.5	970	13	B0945847	B0945847	c 590	17	6.5	200	10	AM522327	AM522327 UI-R-B00-
534	17	6.5	985	29	CG215171	CG215171	c 591	17	6.5	200	10	BB568419	BB568419
535	17	6.5	1001	14	CA471037	CA471037	c 592	17	6.5	202	9	A1136936	A1136936 UI-R-C2P-
536	17	6.5	1015	13	B0934321	B0934321	c 593	17	6.5	204	28	A2990332	A2990332 2M0274EB5
537	17	6.5	1019	28	CC282360	CC282360	594	17	6.5	205	10	BF606142	BF606142 273101.NA
538	17	6.5	1024	29	CNS01578	CG282360	595	17	6.5	208	12	BM842177	BM842177 K-EST0119
539	17	6.5	1028	28	CC304758	CC304758	596	17	6.5	209	14	CA752421	CA752421 UI-M-F00-
540	17	6.5	1029	28	CC224470	CC224470	c 597	17	6.5	213	12	BG382038	BG382038 297756.NA
541	17	6.5	1033	29	CG907498	CG907498	598	17	6.5	213	28	B2662851	B2662851 SALK 0263
542	17	6.5	1033	29	CNS03DJ6	AL239163 Tetraodon	599	17	6.5	216	28	B2596216	B2596216 SALK 0922
543	17	6.5	1041	28	CC214449	CC214449	600	17	6.5	220	28	A2068971	A2068971 RPCT-23-4
544	17	6.5	1045	12	BG295556	BG295556	c 601	17	6.5	221	14	CD803193	CD803193 UI-M-GVO-
545	17	6.5	1094	28	CC273352	CC273352	c 602	17	6.5	223	14	F09079	F09079 HSC2WF092 n
546	17	6.5	1158	12	BG539949	BG539949	c 603	17	6.5	224	10	BB092003	BB092003 BB092003
547	17	6.5	1167	29	CG746243	CG746243	c 604	17	6.5	224	10	BB473846	BB473846 BB473846
548	17	6.5	1197	28	CC261180	CC261180	c 605	17	6.5	227	9	A1561506	A1561506 w92a06.x
549	17	6.5	1201	14	CK028287	CK028287	c 606	17	6.5	227	10	AM524661	AM524661 UI-R-B00-
550	17	6.5	1204	29	CG750473	CG750473	c 607	17	6.5	227	14	CD090629	CD090629 MCL-0076U
551	17	6.5	1212	12	BM4549314	BM4549314	608	17	6.5	227	28	BH848543	BH848543 SALK 0685
552	17	6.5	1230	28	CC189151	CC189151	609	17	6.5	227	29	CE775871	CE775871 t14t-gss-
553	17	6.5	1234	12	B1686981	B1686981	610	17	6.5	229	10	BM150997	BM150997
554	17	6.5	1253	29	CG748711	CG748711	c 611	17	6.5	229	12	BM284893	BM284893
555	17	6.5	1254	29	BM467495	BM467495	c 612	17	6.5	230	13	BY373672	BY373672
556	17	6.5	1266	29	CG743976	CG743976	c 613	17	6.5	230	14	CF539542	CF539542 UI-M-GVO-
557	17	6.5	1277	29	CG746704	CG746704	614	17	6.5	233	9	AV332643	AV332643

615	c	615	16	6.1	235	10	BB276208	BB276208	BB276208	672	16	6.1	283	28	BH012313	BH012313	TDCaH827H
616	c	616	16	6.1	235	12	B0038323	B0038323	Pgn1c.PX0	673	16	6.1	284	29	CE817331	CE817331	tlgr-gss-
617	c	617	16	6.1	236	9	AV322814	AV322814	AV322814	674	16	6.1	285	14	H88375	H88375	ym21603.a1
618	c	618	16	6.1	237	9	A1232819	A1232819	EST229507	675	16	6.1	287	10	BB472147	BB472147	BB472147
619	c	619	16	6.1	237	9	AV336113	AV336113	AV336113	676	16	6.1	287	14	R75424	R75424	MHB0592.Mou
620	c	620	16	6.1	237	29	CE792669	CE792669	tlgr-gss-	677	16	6.1	288	10	BB179748	BB179748	BB179748
621	c	621	16	6.1	237	29	CNS07ERT	Al607619	Anopheles	678	16	6.1	288	10	BB181903	BB181903	BB181903
622	c	622	16	6.1	239	9	AV242121	AV242121	AV242121	679	16	6.1	289	10	AM910708	AM910708	AM910708
623	c	623	16	6.1	243	9	AU229087	AU229087	AU229087	680	16	6.1	289	10	BB071482	BB071482	BB071482
624	c	624	16	6.1	243	9	AA282595	AA282595	zc13f03.s	681	16	6.1	289	10	BB194854	BB194854	BB194854
625	c	625	16	6.1	243	10	BB000141	BB000141	BB000141	682	16	6.1	289	13	BB732670	BB732670	BB732670
626	c	626	16	6.1	246	28	BB48499	BB48499	CIT-HSP-201	683	16	6.1	289	28	AQ086513	AQ086513	HS.Z169.B
627	c	627	16	6.1	247	9	AV244424	AV244424	AV244424	684	16	6.1	290	10	BB174457	BB174457	BB174457
628	c	628	16	6.1	247	10	BB077321	BB077321	BB077321	685	16	6.1	290	10	BB298830	BB298830	BB298830
629	c	629	16	6.1	247	10	BB438388	BB438388	BB438388	686	16	6.1	290	10	BB485919	BB485919	BB485919
630	c	630	16	6.1	248	10	BF555421	BF555421	BF555421	687	16	6.1	290	14	H88389	H88389	BM5103.a1
631	c	631	16	6.1	249	9	AV244424	AV244424	AV244424	688	16	6.1	290	28	AZ882146	AZ882146	RPCI-23-1
632	c	632	16	6.1	251	9	AA002435	AA002435	mg54q04.f	689	16	6.1	291	10	BB003244	BB003244	BB003244
633	c	633	16	6.1	253	9	AV221200	AV221200	AV221200	690	16	6.1	291	10	BB193034	BB193034	BB193034
634	c	634	16	6.1	254	9	AV983111	AV983111	AV983111	691	16	6.1	291	10	BB245374	BB245374	BB245374
635	c	635	16	6.1	254	10	BB428157	BB428157	BB428157	692	16	6.1	291	10	BB489864	BB489864	BB489864
636	c	636	16	6.1	255	28	A2236346	A2236346	RPCI-23-6	693	16	6.1	291	10	BB540456	BB540456	BB540456
637	c	637	16	6.1	255	28	BB859539	BB859539	BB859539	694	16	6.1	292	9	AV242674	AV242674	BB485886
638	c	638	16	6.1	255	28	BB859542	BB859542	B5.08463	695	16	6.1	293	9	A1556095	A1556095	AT556095
639	c	639	16	6.1	256	13	BB633276	BB633276	BB633276	696	16	6.1	293	28	AQ066482	AQ066482	HS.Z247.A
640	c	640	16	6.1	260	10	BB384549	BB384549	BB384549	697	16	6.1	293	10	BF457600	BF457600	BF457600
641	c	641	16	6.1	261	12	BB601362	BB601362	BB601362	698	16	6.1	294	10	BB361858	BB361858	BB361858
642	c	642	16	6.1	262	28	B2680871	B2680871	PUBA3847D	699	16	6.1	294	10	BB571738	BB571738	BB571738
643	c	643	16	6.1	263	10	BF818812	BF818812	QV2-C1010	700	16	6.1	294	10	BB571738	BB571738	BB571738
644	c	644	16	6.1	264	10	BF198277	BF198277	248037.MA	701	16	6.1	295	9	AV225010	AV225010	AV225010
645	c	645	16	6.1	265	29	CE103553	CE103553	tlgr-gss-	702	16	6.1	295	10	BB259346	BB259346	BB259346
646	c	646	16	6.1	266	12	BB141241	BB141241	BB141241	703	16	6.1	296	9	AA916798	AA916798	AA916798
647	c	647	16	6.1	266	28	BB264355	BB264355	BB264355	704	16	6.1	297	12	BG938881	BG938881	BG938881
648	c	648	16	6.1	267	13	BB913747	BB913747	BB913747	705	16	6.1	297	28	CC158095	CC158095	CC158095
649	c	649	16	6.1	268	10	BB066539	BB066539	BB066539	706	16	6.1	299	10	BB061758	BB061758	BB061758
650	c	650	16	6.1	269	9	A1289932	A1289932	qy02h06.x	707	16	6.1	300	13	BY368362	BY368362	BY368362
651	c	651	16	6.1	270	13	BK557419	BK557419	BK557419	708	16	6.1	300	28	AZ092347	AZ092347	AZ092347
652	c	652	16	6.1	270	29	CE603372	CE603372	tlgr-gss-	709	16	6.1	301	29	CG701034	CG701034	CG701034
653	c	653	16	6.1	271	9	AJ005947	AJ005947	AJ005947	710	16	6.1	303	13	C20970	C20970	C20970
654	c	654	16	6.1	272	9	A1854774	A1854774	UI-M-BH0-	711	16	6.1	303	28	B2233559	B2233559	B2233559
655	c	655	16	6.1	274	28	A2492312	A2492312	1M0326D24	712	16	6.1	304	10	BB493246	BB493246	BB493246
656	c	656	16	6.1	274	29	CE123258	CE123258	tlgr-gss-	713	16	6.1	305	10	BB101640	BB101640	BB101640
657	c	657	16	6.1	275	10	BB422254	BB422254	BB422254	714	16	6.1	305	29	CE388645	CE388645	CE388645
658	c	658	16	6.1	275	10	BB431551	BB431551	BB431551	715	16	6.1	308	9	AA268402	AA268402	AA268402
659	c	659	16	6.1	276	9	AV011865	AV011865	AV011865	716	16	6.1	309	10	BB828214	BB828214	BB828214
660	c	660	16	6.1	276	10	BB469644	BB469644	BB469644	717	16	6.1	309	29	CG699293	CG699293	CG699293
661	c	661	16	6.1	276	12	BB161695	BB161695	RE01132.3	718	16	6.1	309	29	BX532606	BX532606	Arb1d0ps
662	c	662	16	6.1	276	13	BY559776	BY559776	BY559776	719	16	6.1	310	10	BB522281	BB522281	BB522281
663	c	663	16	6.1	278	10	BB348942	BB348942	BB348942	720	16	6.1	310	12	BG601360	BG601360	BG601360
664	c	664	16	6.1	278	10	BB528451	BB528451	BB528451	721	16	6.1	311	10	BB335684	BB335684	BB335684
665	c	665	16	6.1	279	12	BB283253	BB283253	UI-R-DD0-	722	16	6.1	311	12	BB293139	BB293139	BB293139
666	c	666	16	6.1	279	29	CG427327	CG427327	0150745-0	723	16	6.1	312	10	AM242368	AM242368	AM242368
667	c	667	16	6.1	281	10	BB441508	BB441508	BB441508	724	16	6.1	312	10	BB520619	BB520619	BB520619
668	c	668	16	6.1	282	12	BB499662	BB499662	UI-H-D10-	725	16	6.1	312	10	BB669538	BB669538	BB669538
669	c	669	16	6.1	283	10	BB143340	BB143340	BB143340	726	16	6.1	312	13	EX618380	EX618380	EX618380
670	c	670	16	6.1	283	10	BB456081	BB456081	BB456081	727	16	6.1	313	9	A1426214	A1426214	mh98602.x
671	c	671	16	6.1	283	12	BB316370	BB316370	BB316370	728	16	6.1	313	10	AM939834	AM939834	CMI-DT008

729	16	6.1	314	28	A0515895	c 786	16	6.1	360	10	BE987780
730	16	6.1	315	9	AV101041	c 787	16	6.1	360	13	C39911
731	16	6.1	315	12	B1687854	c 788	16	6.1	360	14	C43346
732	16	6.1	316	10	BB449185	c 789	16	6.1	360	14	CD956378
733	16	6.1	317	13	C91101	c 790	16	6.1	360	14	CD966541
734	16	6.1	319	9	A1620600	c 791	16	6.1	360	29	CE092280
735	16	6.1	320	9	AV169380	c 792	16	6.1	361	10	AM703423
736	16	6.1	320	29	CE068270	c 793	16	6.1	361	14	CD951371
737	16	6.1	320	29	CE452881	c 794	16	6.1	362	12	BG630512
738	16	6.1	321	10	A1545247	c 795	16	6.1	363	9	AA827458
739	16	6.1	321	10	BB501838	c 796	16	6.1	363	10	BB813807
740	16	6.1	322	10	BB394532	c 797	16	6.1	363	10	BB805158
741	16	6.1	322	29	CE681502	c 798	16	6.1	363	10	BB813807
742	16	6.1	324	10	BB390796	c 799	16	6.1	363	10	BB813807
743	16	6.1	325	9	AV311754	c 800	16	6.1	363	10	BB813807
744	16	6.1	328	10	AA230071	c 801	16	6.1	366	12	BM979415
745	16	6.1	329	14	F07713	c 802	16	6.1	366	29	CE276561
746	16	6.1	329	28	AQ200799	c 803	16	6.1	367	10	BB805158
747	16	6.1	330	9	AA911124	c 804	16	6.1	367	10	BE098176
748	16	6.1	330	9	AI501178	c 805	16	6.1	367	12	BG625879
749	16	6.1	330	9	AL039771	c 806	16	6.1	367	13	BY020527
750	16	6.1	330	9	AV555698	c 807	16	6.1	368	9	AL644003
751	16	6.1	332	9	AA775636	c 808	16	6.1	369	13	BY019879
752	16	6.1	332	10	BB369273	c 809	16	6.1	369	29	CE138776
753	16	6.1	332	12	B1289163	c 810	16	6.1	369	29	CE138776
754	16	6.1	333	9	AT001772	c 811	16	6.1	370	9	AI085557
755	16	6.1	334	14	H33846	c 812	16	6.1	371	10	AM790444
756	16	6.1	335	10	BB678042	c 813	16	6.1	371	12	BG877563
757	16	6.1	337	9	A1422429	c 814	16	6.1	371	29	CE695680
758	16	6.1	337	28	B2919454	c 815	16	6.1	372	10	BF721900
759	16	6.1	338	9	AA877003	c 816	16	6.1	373	10	BB837033
760	16	6.1	338	10	BB099450	c 817	16	6.1	373	10	BB837033
761	16	6.1	339	28	BB810757	c 818	16	6.1	375	28	BH712714
762	16	6.1	340	9	A1234909	c 819	16	6.1	375	28	AQ377405
763	16	6.1	340	10	BB121349	c 820	16	6.1	377	9	AA989172
764	16	6.1	341	10	AA954653	c 821	16	6.1	377	10	AM295607
765	16	6.1	341	10	BG070139	c 822	16	6.1	377	10	BB800745
766	16	6.1	342	10	BB100294	c 823	16	6.1	378	13	BK726351
767	16	6.1	342	28	A2560216	c 824	16	6.1	379	13	BY482004
768	16	6.1	344	12	BG372664	c 825	16	6.1	379	29	CE619823
769	16	6.1	346	12	B1966004	c 826	16	6.1	379	29	CE635882
770	16	6.1	346	28	AQ028531	c 827	16	6.1	380	12	B1966171
771	16	6.1	346	28	AQ223380	c 828	16	6.1	380	12	B0316159
772	16	6.1	347	9	A1290680	c 829	16	6.1	380	14	243542
773	16	6.1	347	9	AV693524	c 830	16	6.1	381	10	BB793278
774	16	6.1	347	12	BG100453	c 831	16	6.1	381	28	AZ248227
775	16	6.1	347	12	B1294552	c 832	16	6.1	382	28	BH291646
776	16	6.1	350	10	BB843821	c 833	16	6.1	384	29	AG261312
777	16	6.1	350	10	BB843821	c 834	16	6.1	384	13	BY701363
778	16	6.1	354	9	AA250216	c 835	16	6.1	385	9	A1764253
779	16	6.1	354	10	BB258374	c 836	16	6.1	385	10	AM948637
780	16	6.1	354	28	AZ892139	c 837	16	6.1	385	29	CG861219
781	16	6.1	354	28	BH445456	c 838	16	6.1	387	10	AM413754
782	16	6.1	356	10	BB241758	c 839	16	6.1	387	10	BB837489
783	16	6.1	356	12	BM940697	c 840	16	6.1	387	12	BM356370
784	16	6.1	358	28	BB860351	c 841	16	6.1	387	13	BY483341
785	16	6.1	359	28	B2761307	c 842	16	6.1	388	10	AM948571

843	16	6.1	388	14	CA488005	CA488005	AGENCYCOURT	900	16	6.1	412	10	BF389768	BF389768	UI-R-B52-
c 844	16	6.1	389	9	AA997771	AA997771	UI-R-EO-d	c 901	16	6.1	413	10	BB731719	BB731719	BB731719
c 845	16	6.1	389	9	A1298882	A1298882	qm99410.x	c 902	16	6.1	414	10	AM206511	AM206511	UI-H-B11-
c 846	16	6.1	389	28	B30832	B30832	HS-1003-A2-	c 903	16	6.1	414	29	BX532605	BX532605	HS-1003-A2-
c 847	16	6.1	390	10	AA524847	AA524847	UI-R-B00-	c 904	16	6.1	415	14	CA847219	CA847219	UI-R-B00-
c 848	16	6.1	391	9	AA668081	AA668081	ak44606.s	c 905	16	6.1	415	14	CP426321	CP426321	UI-R-B00-
c 849	16	6.1	391	9	AA900710	AA900710	UI-R-EO-b	c 906	16	6.1	415	28	AO5356970	AO5356970	HS-5308-B
c 850	16	6.1	392	10	AA944638	AA944638	QVO-F7000	c 907	16	6.1	415	28	AO585606	AO585606	RPCI-11-4
c 851	16	6.1	392	10	BB843399	BB843399	CMO-TN003	c 908	16	6.1	415	29	CE084456	CE084456	UI-R-gsa-
c 852	16	6.1	392	14	CD972253	CD972253	QAE1c11.y	c 909	16	6.1	417	29	CE645485	CE645485	UI-R-gsa-
c 853	16	6.1	393	9	A1501988	A1501988	UI-R-EO-d	c 910	16	6.1	417	29	CE762634	CE762634	UI-R-gsa-
c 854	16	6.1	393	9	AV591094	AV591094	AV591094	c 911	16	6.1	418	28	AO523588	AO523588	UI-R-gsa-
c 855	16	6.1	396	29	CC781529	CC781529	ZMWBEO43	c 912	16	6.1	420	12	BE660341	BE660341	UI-R-gsa-
c 856	16	6.1	398	10	BE172065	BE172065	MRO-HT055	c 913	16	6.1	421	9	A1413338	A1413338	mc90e01.x
c 857	16	6.1	398	29	CG737389	CG737389	ZMWBEO32	c 914	16	6.1	422	28	AO134340	AO134340	UI-R-gsa-
c 858	16	6.1	399	9	A1025142	A1025142	ou55h11.x	c 915	16	6.1	423	12	BM390226	BM390226	UI-R-CN1-
c 859	16	6.1	399	10	BB817975	BB817975	BY701536	c 916	16	6.1	423	12	BM390226	BM390226	UI-R-CN1-
c 860	16	6.1	399	13	BY701536	BY701536	BY701536	c 917	16	6.1	424	12	BM390226	BM390226	UI-R-CN1-
c 861	16	6.1	399	28	BH126595	BH126595	BANC-SatC	c 918	16	6.1	424	29	CE097104	CE097104	UI-R-gsa-
c 862	16	6.1	400	10	BE446709	BE446709	WHE1139.C	c 919	16	6.1	425	10	BE203681	BE203681	UI-R-gsa-
c 863	16	6.1	401	10	AA430671	AA430671	70539.MAR	c 920	16	6.1	425	14	CD465307	CD465307	UI-R-gsa-
c 864	16	6.1	401	10	BB682808	BB682808	BB682808	c 921	16	6.1	425	14	CD465307	CD465307	UI-R-gsa-
c 865	16	6.1	401	13	BY632469	BY632469	BY632469	c 922	16	6.1	425	29	CE302622	CE302622	UI-R-gsa-
c 866	16	6.1	401	29	CE540332	CE540332	UI-R-gsa-	c 923	16	6.1	426	9	A1413407	A1413407	UI-R-gsa-
c 867	16	6.1	401	29	AL755941	AL755941	ArbIdops	c 924	16	6.1	426	10	BB677625	BB677625	UI-R-gsa-
c 868	16	6.1	402	29	CC911129	CC911129	ZMWBEO36	c 925	16	6.1	426	28	CC054809	CC054809	UI-R-gsa-
c 869	16	6.1	403	13	BA094465	BA094465	BA094465	c 926	16	6.1	427	9	A1348628	A1348628	q035a10.x
c 870	16	6.1	403	13	BK512748	BK512748	BK512748	c 927	16	6.1	427	10	BB733371	BB733371	UI-R-gsa-
c 871	16	6.1	403	28	AQ716761	AQ716761	HS-5463.A	c 928	16	6.1	428	13	BY447966	BY447966	UI-R-gsa-
c 872	16	6.1	404	10	AA311704	AA311704	5526.MAR	c 929	16	6.1	428	13	BZ594076	BZ594076	UI-R-gsa-
c 873	16	6.1	404	10	BB797863	BB797863	BB797863	c 930	16	6.1	429	9	AA648705	AA648705	UI-R-gsa-
c 874	16	6.1	404	14	CB242048	CB242048	UI-CF-FNO	c 931	16	6.1	429	13	BY538049	BY538049	UI-R-gsa-
c 875	16	6.1	405	10	AA636034	AA636034	108087.MA	c 932	16	6.1	429	13	BY538049	BY538049	UI-R-gsa-
c 876	16	6.1	405	10	AA656055	AA656055	108087.MA	c 933	16	6.1	429	13	BY538049	BY538049	UI-R-gsa-
c 877	16	6.1	405	28	AQ338491	AQ338491	HS-3118.B	c 934	16	6.1	429	14	H96813	H96813	UI-R-gsa-
c 878	16	6.1	406	9	A198641	A198641	tm47b04.x	c 935	16	6.1	429	29	EP014103U	EP014103U	UI-R-gsa-
c 879	16	6.1	406	10	BF588969	BF588969	BF588969	c 936	16	6.1	430	9	AA879273	AA879273	UI-R-gsa-
c 880	16	6.1	406	28	AQ338532	AQ338532	HS-3118.B	c 937	16	6.1	430	10	AM707156	AM707156	UI-R-gsa-
c 881	16	6.1	406	28	CC056376	CC056376	SALK-1033	c 938	16	6.1	430	10	BB774775	BB774775	UI-R-gsa-
c 882	16	6.1	407	9	AV590736	AV590736	AV590736	c 939	16	6.1	430	14	CA536585	CA536585	UI-R-gsa-
c 883	16	6.1	407	10	BF71028	BF71028	IL5-IT002	c 940	16	6.1	431	14	CA536585	CA536585	UI-R-gsa-
c 884	16	6.1	407	10	BF904165	BF904165	MR3-MT032	c 941	16	6.1	431	29	CE838375	CE838375	UI-R-gsa-
c 885	16	6.1	408	10	BF754330	BF754330	IL5-CF051	c 942	16	6.1	432	9	A1359112	A1359112	UI-R-gsa-
c 886	16	6.1	408	12	BF934216	BF934216	EST554105	c 943	16	6.1	432	10	BB828493	BB828493	UI-R-gsa-
c 887	16	6.1	408	28	AA144134	AA144134	HS-3074.A	c 944	16	6.1	432	10	BE945834	BE945834	UI-M-B20-
c 888	16	6.1	408	28	AA610255	AA610255	HS-5094.A	c 945	16	6.1	432	12	BI293336	BI293336	UI-R-DKO-
c 889	16	6.1	409	9	AV590062	AV590062	AV590062	c 946	16	6.1	432	28	AZ443104	AZ443104	1M0237E08
c 890	16	6.1	409	10	BB829007	BB829007	BB829007	c 947	16	6.1	433	10	BF958320	BF958320	UI-R-gsa-
c 891	16	6.1	409	12	BB789371	BB789371	SEAMC009	c 948	16	6.1	434	9	A1033955	A1033955	UI-R-gsa-
c 892	16	6.1	409	28	BE160744	BE160744	HS-5009.A	c 949	16	6.1	434	28	BB332429	BB332429	UI-R-gsa-
c 893	16	6.1	410	9	AA337143	AA337143	oo98g05.s	c 950	16	6.1	434	28	BH859238	BH859238	UI-R-gsa-
c 894	16	6.1	410	10	AA944636	AA944636	QVO-F7000	c 951	16	6.1	435	9	AM057697	AM057697	UI-R-gsa-
c 895	16	6.1	410	12	BG554898	BG554898	dac3f02.	c 952	16	6.1	435	10	BB823948	BB823948	UI-R-gsa-
c 896	16	6.1	411	10	AA650803	AA650803	EST329257	c 953	16	6.1	435	10	BE097149	BE097149	UI-R-gsa-
c 897	16	6.1	411	10	BB733419	BB733419	BB733419	c 954	16	6.1	435	29	CE564116	CE564116	UI-R-gsa-
c 898	16	6.1	411	28	BH338096	BH338096	CH230-89D	c 955	16	6.1	436	28	AO197385	AO197385	CIT-gsa-2

c 957	16	6.1	436	28	AQ280094	AQ280094	CITBI-EI-
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c 959	16	6.1	437	9	AA729577	AA729577	rx36g10.s
c 960	16	6.1	437	9	AA621194	AA621194	zu81b06.s
c 961	16	6.1	437	14	CF047804	CF047804	QC13c12.
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c 963	16	6.1	439	9	AU023617	AU023617	AU023617
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c 965	16	6.1	440	9	AA489045	AA489045	aa56d08.s
c 966	16	6.1	440	10	BB822178	BB822178	BB822178
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c 969	16	6.1	441	9	AA648385	AA648385	ns21e04.s
c 970	16	6.1	441	9	AA151572	AA151572	z128e04.s
c 971	16	6.1	441	9	AA530985	AA530985	nj10h05.s
c 972	16	6.1	441	10	BB732340	BB732340	BB732340
c 973	16	6.1	442	12	B1185862	B1185862	UNL-P-FN-
c 974	16	6.1	442	12	BJ209857	BJ209857	BJ209857
c 975	16	6.1	442	14	R94319	R94319	yq41e08.r1
c 976	16	6.1	442	29	CE695445	CE695445	tl9f-gs-
c 977	16	6.1	443	9	AU229859	AU229859	AU229859
c 978	16	6.1	444	9	AI852447	AI852447	UI-M-BH0-
c 979	16	6.1	444	13	BK630615	BK630615	BK630615
c 980	16	6.1	444	13	BY482671	BY482671	BY482671
c 981	16	6.1	445	9	AI242519	AI242519	qu36e01.x
c 982	16	6.1	445	14	CA321131	CA321131	UI-M-FW0-
c 983	16	6.1	446	9	AI818030	AI818030	wK41e04.x
c 984	16	6.1	446	10	AW853416	AW853416	RC1-CT025
c 985	16	6.1	446	10	BE417602	BE417602	MUG022.G0
c 986	16	6.1	446	13	BY572097	BY572097	BY572097
c 987	16	6.1	448	10	BF416593	BF416593	UI-R-CAL-
c 988	16	6.1	448	10	BB761380	BB761380	BB761380
c 989	16	6.1	448	28	AQ534775	AQ534775	RPCI-11-3
c 990	16	6.1	448	29	CG029636	CG029636	CHGA067TF
c 991	16	6.1	449	9	AI509163	AI509163	mh98e02.y
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c 996	16	6.1	451	13	BQ370547	BQ370547	CM1-GN028
c 997	16	6.1	451	13	BQ560915	BQ560915	H4067C05-
c 998	16	6.1	452	9	AI401684	AI401684	th24g03.x
c 999	16	6.1	452	9	AI653579	AI653579	tg96e11.x
c 1000	16	6.1	452	9	AW082926	AW082926	xc04e08.x

Search completed: October 15, 2004, 06:26:08
Job time : 1285.86 secs

OM nucleole - nucleole search, using SW model

Run on: October 14, 2004, 09:12:14 ; Search time 3665.14 Seconds
(without alignments)

8443.595 Million cell updates/sec

Title: US-09-407-804A-4

Perfect score: 714
Sequence: 1 atgacgcatactatagaaaa.....agatccctgataaagtga 714

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_hcg: +
3: gb_in: +
4: gb_ov: +
5: gb_ov: +
6: gb_pac: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_re: +
11: gb_scs: +
12: gb_sy: +
13: gb_un: +
14: gb_vi: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_ov: +
21: em_ov: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_scs: +

28: em_un: +
29: em_vi: +
30: em_hcg_hum: +
31: em_hcg_inv: +
32: em_hcg_other: +
33: em_hcg_mus: +
34: em_hcg_pin: +
35: em_hcg_rnd: +
36: em_hcg_mam: +
37: em_hcg_vrt: +
38: em_sy: +
39: em_hcgo_hum: +
40: em_hcgo_mus: +
41: em_hcgo_other: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	ID	
1	714	100.0	714	6	BD245275
2	714	100.0	41708	6	BD245281
3	714	100.0	41708	6	AR368770
4	109.8	15.4	170627	2	AC125567
5	107.8	15.1	175544	2	AC117342
6	94	13.2	161398	2	AC092804
7	93	13.0	195620	2	BX088600
8	92.6	13.0	104992	2	AC005504
9	92.6	13.0	169546	2	AC004157
10	92.6	13.0	250421	2	AE014849
11	92.2	12.9	99003	2	AL390756
12	91.4	12.8	89665	9	AC063976
13	91.4	12.8	163660	2	AC046165
14	91.4	12.8	218083	2	AC142177
15	90.8	12.7	2452	3	AF337815
16	90.4	12.7	349980	6	AX344555
17	90.2	12.6	131682	9	AL672277
18	90.2	12.6	152651	2	BX322643
19	90	12.6	250713	3	AE014850
20	89.8	12.6	246611	2	AC111404
21	89.4	12.5	250743	3	AE014836
22	89.2	12.5	157141	3	AC016445
23	89	12.5	1219	3	AF513853
24	89	12.5	250029	3	AE014820
25	88.8	12.4	159618	9	AC096730
26	88.8	12.4	169122	9	AC106803
27	88.8	12.4	254050	3	PF929338
28	88.4	12.4	313050	3	PF929332
29	88.2	12.4	250029	3	AE014839
30	88	12.3	192265	9	CNS01893
31	87.8	12.3	14867	3	AE001398
32	87.6	12.3	8056	6	AX598900
33	87.6	12.3	8056	6	AX599046

c	34	87.4	12.2	1453	8	AL551978	Arbipod
c	35	87.4	12.2	137889	9	AC073269	Homo sapi
c	36	87.4	12.2	369751	3	PFMLA932	Plasmodi
	37	87.2	12.2	47601	9	AC078892	Plasmodi
	38	87.2	12.2	66442	9	PFMLA174	Homo sapi
	39	87.2	12.2	195620	2	EX088600	Danio rerio
c	40	87	12.2	3683	6	AL551989	Sequence
	41	86.6	12.1	90550	9	AL552166	Human DNA
	42	86.6	12.1	156723	3	AL010838	Drosophila
	43	86.6	12.1	312724	3	AE003846	Drosophila
c	44	86.4	12.1	39575	3	AL116925	Drosophila
	45	86.4	12.1	250823	3	AE014821	Plasmodi

ALIGNMENTS

	714 bp	DNA	linear PAT 17-JUI-2003
RESULT 1 BD245275	BD245275		
LOCUS	Development of novel antibiotics based on bacteriophage genomics.		
DEFINITION	BD245275		
ACCESSION	BD245275.1 GI:33055045		
VERSION	CP 2002531107-A/10.		
KEYWORDS	unidentified		
SOURCE	unclassified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 714)		
AUTHORS	Pelletier,J., Gros,P. and Dubow,M.		
TITLE	Development of novel antibiotics based on bacteriophage genomics		
JOURNAL	Patent; CP 2002531107-A 10 24-SEP-2002;		

COMMENT	
OS	Staphylococcus aureus bacteriophage 77
PN	JP 200251107-A/10
PD	24-SEP-2002
PF	03-DEC-1999 JP 2000585456
PR	03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US	09/407804, 30-SEP-1999 US 60/157218 PR
11-DEC-1999 US	60/168777, 02-DEC-1999 US 09/454252 PT JERRAY
PUBLISHER	PHILLIPPE GROS, MICHAEL DUBOW
PC	C12N15/09, A61N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005, PC
PC	C12M1/00,
PC	C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,	
PC	A61K37/02
CC	Coding Sequence
FH	Key
FT	source
FT	1. 714
FT	/organism="Staphylococcus
aureus bacteriophage	77".
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	/mol_type="genomic DNA"
	/db_xref="cacon:32644"
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	QY	241	AAGGAGATATAGTAATCTATTCCCTATCCTCAAAAGAAAACAAAAAGATTAAAG	300
	Dd	23742	AAGGAGATATAGTAATCTATTCCCTATCCTCAAAAGAAAACAAAATATTAAAG	23682
	QY	301	ATGAATTTTGAATGGAAATGGAGATATTATTAGAATGTGTTTTAAATTAATTAGCGCG	360
	Dd	23682	ATGAATTTTGAATGGAAATGGAGATATTATTAGAATGTGTTTTAAATTAATTAGCGCG	23622
	QY	361	CAAAATATTCAGCATATTAAAGAAAGTTTGATTAATAAATATCACAAAACACACA	420
	Dd	23622	CAAAATATTCAGCATATTAAAGAAAGTTTGATTAATAAATATCACAAAACACACACA	23562
	QY	421	GAAATTCACACTAAAGATTAATTTTATGGAATTTATCTGAATGTTAGAAATGAAAT	480
	Dd	23562	GAAATTCACACTAAAGATTAATTTTATGGAATTTATCTGAATGTTAGAAATGAAAT	23502
	QY	481	AAATTAATTAATTAATTCAGCAAACATTAATAACATATGTCAGCATATGATAAGTAAA	540
	Dd	23502	AAATTAATTAATTAATTCAGCAAACATTAATAACATATGTCAGCATATGATAAGTAAA	23442
	QY	541	AAATTAATTAATTAATGTAAGCTTGCAATTAATCTTTCACGCATTAAGTAGTTGCG	600
	Dd	23442	AAATTAATTAATTAATGTAAGCTTGCAATTAATCTTTCACGCATTAAGTAGTTGCG	23382
	QY	601	ATAAGAAAGTTTATGCCCAAAAATTAAAAATCCAGTAAATAGATCTTCOSGATATATG	660
	Dd	23382	ATAAGAAAGTTTATGCCCAAAAATTAAAAATCCAGTAAATAGATCTTCOSGATATATG	23322
	QY	661	TTACTGATTAATAGATTAATTAATAATATTAATTCAGATCCCTGATTAAGATGA	714
	Dd	23322	TTACTGATTAATAGATTAATTAATAATATTAATTCAGATCCCTGATTAAGATGA	23269
RESULT 3				
AR368770/c				
LOCUS	AR368770	41708 bp	DNA	linear PAT 12-SEP-2003
DEFINITION	Sequence 3 from patent US 637652.			
ACCESSION	AR368770			
VERSION	AR368770.1 GI:34603077			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 41708)			
TITLE	Pelletier,J., Gros,P. and Dubou,M.			
JOURNAL	Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein			
FEATURES	Patent: US 637652-A 3 23-Apr-2002;			
source	Location/Qualifiers			
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Best Local Similarity	100.0%; Pred. No. 1,2e+82;			

Search completed: October 14, 2004, 16:00:15
Job time : 3672.14 secs

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c	714	100.0	41708	4	AA68106	Complete
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5	87.6	12.3	8036	7	AB210100	Haematop
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c	87	12.2	3633	7	AB210199	Human br

8	86.2	12.1	700	4	AAH93026	AbH93026 Human inf
9	84.8	11.9	15674	6	ABJ32363	AbJ32363 Human imm
10	84.8	11.9	15674	6	ABJ34477	AbJ34477 Human met
11	84.8	11.9	15674	6	ABJ70514	AbJ70514 Chemcall
12	83.8	11.7	6375	6	ABJ34025	AbJ34025 Human imm
13	83.8	11.7	38342	4	AA546746	AA546746 Tumour su
14	83.8	11.7	38342	6	ABK31507	AbK31507 Signal tr
15	83	11.6	61020	4	AA546788	AA546788 Tumour su
16	81	11.3	6292	4	AA546735	AA546735 Tumour su
17	80.6	11.3	9741	6	ABJ33323	AbJ33323 Human imm
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19	80	11.2	17538	6	ABJ33157	AbJ33157 Human imm
20	79.6	11.1	7351	6	ABJ32028	AbJ32028 Human imm
21	79	11.1	3683	7	ABZ10053	AbZ10053 Haematopo
22	78.8	11.0	18154	6	ABJ32254	AbJ32254 Human imm
23	78.4	11.0	18218	6	ABJ33949	AbJ33949 Human imm
24	78.2	11.0	83391	6	ABQ67093	AbQ67093 Human ang
25	77.8	10.9	8056	7	ABZ10246	AbZ10246 Haematopo
26	77	10.8	2501	9	ADB54244	ADB54244 Pretreate
27	77	10.8	5689	4	AA545384	AA545384 Chemcall
28	77	10.8	5689	4	AA546426	AA546426 Tumour su
29	77	10.8	5689	6	ABK28226	AbK28226 DNA trans
30	77	10.8	8056	7	ABZ10100	AbZ10100. Haematopo
31	76.8	10.8	9539	4	AA545346	AA545346 Chemcall
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35	76	10.6	6644	2	AAK33181	AAK33181 Base sequ
36	76	10.6	7372	2	AAK33182	AAK33182 Base sequ
37	76	10.6	7797	2	AAK33180	AAK33180 Compox vl
38	76	10.6	7996	2	AAK33184	AAK33184 Base sequ
39	76	10.6	14006	6	ABJ33958	AbJ33958 Human imm
40	75.8	10.6	6856	6	ABJ70225	AbJ70225 Chemcall
41	75.6	10.6	6898	6	ABH80222	AbH80222 Human che
42	75.6	10.6	13511	6	ABJ32281	AbJ32281 Human imm
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44	75.4	10.6	6095	4	AA546310	AA546310 Tumour su
45	75.4	10.6	6095	6	ABJ32361	AbJ32361 Human imm

ALIGNMENTS

RESULT 1
AAA68248
ID **AAA68248** standard; DNA; 714 BP.
XX
AC **AAA68248;**
XX
DT **15-SEP-2003** (revised)
DT **06-AUG-2003** (revised)
DT **27-OCT-2000** (first entry)
XX
DE **Bacteriophage 77 77ORF017** nucleotide sequence.
XX
KW **Bacteriophage; antimicrobial; genome; identification; antibacterial;**
KW **bacterial growth inhibition; bacterial infection; ds.**

XX	Staphylococcus aureus; bacteriophage 77.
OS	WO200032825-A2.
XX	
PN	08-JUN-2000.
XX	
PD	
XX	
PF	03-DEC-1999; 99WO-IB002040.
XX	
PR	03-DEC-1998; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407804.
PR	30-SEP-1999; 99US-0137218P.
PR	01-DEC-1999; 99US-0168777P.
XX	02-DEC-1999; 99US-00454252.
PA	(PHAG-) PHAGEGEN INC.
XX	
PI	Pelletier J, Gros P, Dubow M,
XX	WPI; 2000-412361/35.
DR	P-PSDB; AAB16523.
XX	
PT	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
PT	inhibits bacteria when a bacteriophage infects a bacterium.
XX	
PS	Disclosure; Page 153; 456pp; English.
XX	
CC	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AA68243 to AA69442 and AAB16523 to AAB16954 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC	(Updated on 15-SEP-2003 to standardise OS field.)
XX	
SQ	Sequence 714 BP; 312 A; 77 C; 96 G; 229 T; 0 U; 0 Other;
Query Match	100.0%; Score 714; DB 3; Length 714;
Best Local Similarity	100.0%; Pred. No. 7.8e-101;
Matches 714; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	1 ATGAGCATATATATGAAAAAGCATTAATTAATTAATTAATTAATTCGAAATCCAAATTT 60
OY	61 AAAAGTTAGATTCAGATATTCATATTACTCAAGAGTTGAAGGTGAAAAAACAAT 120
DB	61 AAAAGTTAGATTCAGATATTCATATTACTCAAGAGTTGAAGGTGAAAAAACAAT 120
OY	121 AAAGTTTATCCAAAGTTTAAACAAGAGAAATTAAGTTTGTAGATTGCGTAAAC 180

PD	06-JUN-2000.
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PF	03-DEC-1999; 99WO-IB002040.
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PR	03-DEC-1998; 98US-0110992P.
DR	03-JUN-1999; 99US-00326144.
XX	
PR	28-SEP-1999; 99US-0040780A.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168777P.
PR	02-DEC-1999; 99US-0045425Z.
XX	
PA	(PHAG-) PHAGETECH INC.
PI	Pelletier J, Gros P, Dubow M;
DR	WPI; 2000-412361/35.
PT	
PT	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
PT	inhibits bacteria when a bacteriophage infects a bacterium.
XX	
PS	Example 3; Page 141-151; 456pp; English.
XX	
CC	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AAB68243 to AAB69442 and AB16523 to AB16954 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC	(Updated on 15-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
XX	
BQ	Query Match 100.0%; Score 714; DB 3; Length 41708;
XX	
Best Local Similarity	100.0%; Pred. No. 5,8e+10;
Matches 714;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DQ	
Y	1 ATGACGATATATAGAAAAGCATTTAATAATTAATTAACCTCTGGAAATCCAAATT 60
DQ	23982 ATGACGCAATATATAGAAAAGCATTTAATAATTAATTAACCTCTGGAAATCCAAATT 23922
Y	61 AAAAGTGAATCGAATATTCCTATTACTCAAGAATTGAAGTGAAAAAACAT 120
DQ	23922 AAAAGTGAATCGAATATTCCTATTACTCAAGAATTGAAGTGAAAAAACAT 23863
Y	121 AAAGTTTTATCCAAAGTTAAACAAGAGAAATGTTTTGTAAATTCGGTATAAC 180
DQ	23862 AAAGTTTTATCCAAAGTTAAACAAGAGAAATGTTTTGTAAATTCGGTATAAC 23803
Y	181 GTTATTAAGAAATTTCTATTCCACTTTCGCATAGTAGAATTAATAAGATCTAT 240
DQ	23802 GTTATTAAGAAATTTCTATTCCACTTTCGCATAGTAGAATTAATAAGATCTAT 23744

QY 241 ACGAGATATAGTAATGTTATTCCTTACCTTAAGAAAAAGATTTAAAG 300
DB 23742 ACGAGATATAGTAATGTTATTCCTTACCTTAAGAAAAAGATTTAAAG 23683
QY 301 ATGAATTTGATTGAAATGGAGATTTATTAAGATTTGTTTAAATTAATTAACGCG 360
DB 23682 ATGAATTTGATTGAAATGGAGATTTATTAAGATTTGTTTAAATTAATTAACGCG 23623
QY 361 CAAATATATTCAGCTATATTAAGAGATTTTCGATTAAGAAAAATACCAACACA 420
DB 23622 CAAATATATTCAGCTATATTAAGAGATTTTCGATTAAGAAAAATACCAACACA 23563
QY 421 GAATTCATCACTAAAGATTTTATTTGAATTTATATCTGATAGTTTGAATTTGAAT 480
DB 23562 GAATTCATCACTAAAGATTTTATTTGAATTTATATCTGATAGTTTGAATTTGAAT 23503
QY 481 AATTAATTAATTAATTAAGAGAAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 23502 AATTAATTAATTAATTAAGAGAAATTAATTAATTAATTAATTAATTAATTAATTA 23443
QY 541 AATTAATTAATTAATTAAGATTTACCTTGCATTAATTTCTTCCAGCCGATTAAGTTTCC 600
DB 23442 AATTAATTAATTAATTAAGATTTACCTTGCATTAATTTCTTCCAGCCGATTAAGTTTCC 23383
QY 601 ATAAAGAAAGTTTATCCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 660
DB 23382 ATAAAGAAAGTTTATCCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 23323
QY 661 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 714
DB 23322 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 23269

RESULT 3
AAC86106/c
ID AAC86106 standard; cDNA; 41708 BP.
XX
AC AAC86106;
XX
DT 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
DE Complete genome of bacteriophage 77.
XX
KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW decreasing assay; ss.
XX
OS Bacteriophage.
XX
PN W0200146383-A2.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WC-US035180.
XX
PR 22-DEC-1999; 99US-00470512.

PR 12-OCT-2000; 2000US-00689952.
XX
XX (PHAG-) PHAGE TECH INC.
PA (WILLI) WILLIAMS K M.
XX
XX Pelletier J, Gros P, Dubow M;
DR WPI; 2001-418052/44.
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by Staphylococcus
PT aureus.
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX This sequence represents the genome of Bacteriophage 77. The growth
XX inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcal, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
XX 06-AUG-2003 to correct OS field.)
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 714; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 5.8e-101;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAGCCATTAATTAAGAAAAAGCATTAAATTAATTAATTAATTAATTAATTAATTA 60
DB 23982 ATAGCCATTAATTAAGAAAAAGCATTAAATTAATTAATTAATTAATTAATTAATTA 23923
QY 61 AAAAGTTAGTTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
DB 23922 AAAAGTTAGTTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 23863
QY 121 AAAAGTTTATCCAAAGTTTAAACAAGAAATAGTTTGTAGTTTCGGTAAAC 180
DB 23862 AAAAGTTTATCCAAAGTTTAAACAAGAAATAGTTTGTAGTTTCGGTAAAC 23803
QY 181 GTTAATTAAGATTTTCTAATTCACACTTGCATTAATTAATTAATTAATTAATTAATTA 240
DB 23802 GTTAATTAAGATTTTCTAATTCACACTTGCATTAATTAATTAATTAATTAATTAATTA 23743
QY 241 ACGAGATATAGTAATGTTATTCCTTACCTTAAGAAAAAGATTTAAAG 300
DB 23742 ACGAGATATAGTAATGTTATTCCTTACCTTACCTTAAGAAAAAGATTTAAAG 23683
QY 301 ATGAATTTGATTGAAATGGAGATTTATTAAGATTTGTTTAAATTAATTAATTAACGCG 360
DB 23682 ATGAATTTGATTGAAATGGAGATTTATTAAGATTTGTTTAAATTAATTAATTAACGCG 23623
QY 361 CAAATATATTCAGCTATATTAAGAGATTTTCGATTAAGAAAAATACCAACACA 420

28: gb_gsa1:*

29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	113.6	15.9	1200	13	BK437758	BK437758 BK437758
2	110	15.4	1200	13	BK415878	BK415878 BK415878
3	105	14.7	1101	29	CNS00EVL	AL069706 Drosophila
4	102.2	14.3	1348	29	CG749499	CG749499 P043-4-A0
5	102	14.3	1391	29	CG754863	CG754863 P050-2-G0
6	101.6	14.2	1201	13	BK335216	BK335216 BK335216
7	101.2	14.2	778	29	AG058583	AG058583 Pan trogl
8	100.6	14.1	1201	13	BK420717	BK420717 BK420717
9	100.2	14.0	1626	14	CF238805	CF238805 AGENCOURT
10	100	13.9	1896	29	CG753083	CG753083 P048-1-C0
11	99.6	13.9	1123	14	CD325190	CD325190 AGENCOURT
12	97.6	13.7	1200	13	BK436510	BK436510 BK436510
13	97	13.6	1201	9	AL536104	AL536104 AL536104
14	96.6	13.5	1178	28	BZ696021	BZ696021 SP_Ba007
15	96	13.4	1201	9	AL565455	AL565455 AL565455
16	95.8	13.4	1045	13	BK456814	BK456814 BK456814
17	94.4	13.2	879	29	CNS01JRG	AL147405 Anopheles
18	94.2	13.2	1101	29	CNS0021J	AL061936 Drosophila
19	94	13.2	1201	29	CNS0167M	AL106336 Drosophila
20	93.6	13.1	998	13	BK436885	BK436885 BK436885
21	93.6	13.1	1201	13	BK439779	BK439779 BK439779
22	93.4	13.1	1101	29	CNS00396	AL063921 Drosophila
23	93.2	13.1	964	13	BK341256	BK341256 BK341256
24	93	13.0	1164	28	CC218891	CC218891 CH261-14M
25	92.6	13.0	1092	29	CNS020K7	AL175696 Tetradon
26	92.6	13.0	1202	28	CC262481	CC262481 CH261-167
27	92.4	12.9	1101	29	CNS00EPO	AL069493 Drosophila
28	92	12.9	781	29	CNS009DO	AL053444 Drosophila
29	92	12.9	1074	28	BZ696936	BZ696936 SP_Ba009
30	91.8	12.9	1175	28	BZ696936	BZ696936 SP_Ba008
31	91.8	12.9	1200	13	BK415878	BK415878 BK415878
32	91.8	12.9	1392	29	CG757503	CG757503 P052-4-C0
33	91.6	12.8	910	12	BK415636	BK415636 OP20714 M
34	91.4	12.8	935	28	BI0881	BI0881 F24H6-Sp6.1
35	91.4	12.8	994	29	CNS04NOJ	AL298972 Tetradon
36	91.2	12.8	990	29	CNS00601	AL065624 Drosophila
37	91	12.7	1056	13	BK415058	BK415058 BK415058
38	91	12.7	1190	29	CNS020N7	AL206908 Tetradon
39	91	12.7	1350	29	CG744271	CG744271 P036-4-C0
40	90.8	12.7	1101	29	CNS00E07	AL069440 Drosophila
41	90.6	12.7	1029	29	CNS01ZG4	AL174271 Tetradon
42	90.6	12.7	1169	29	CNS06KHQ	AL402900 T3 end of
43	89.4	12.6	1201	9	AL536104	AL536104 AL536104
44	89.8	12.6	1101	29	CNS00EVL	AL069706 Drosophila
45	89.8	12.6	1193	29	CG745316	CG745316 P038-1-G0

Search completed: October 14, 2004, 18:55:05
Job time : 3339.86 secs

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 ; Search time 3665.45 Seconds
(without alignments)

8442.862 Million cell updates/sec

Title: US-09-407-804A-4

Perfect score: 714

Sequence: 1 atgacgcatacatatagaataa.....agatccctcatatagaatga 714

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_hvg: +
3: gb_in: +
4: gb_ov: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sts: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
15: em_ba: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_sts: +

28: em_un: +
29: em_vl: +
30: em_hvg_hum: +
31: em_hvg_inv: +
32: em_hvg_other: +
33: em_hvg_mus: +
34: em_hvg_pln: +
35: em_hvg_rdt: +
36: em_hvg_mam: +
37: em_hvg_vrt: +
38: em_sy: +
39: em_hvg_hum: +
40: em_hvg_mus: +
41: em_hvg_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	714	100.0	714	BD245275
2	714	100.0	41708	BD245281
3	714	100.0	41708	AR368770
4	24	3.4	45861	DMC80H7
5	24	3.4	62422	AC128735
6	24	3.4	74084	AC017603
7	24	3.4	181360	AC104141
8	24	3.4	206551	AC115789
9	24	3.4	304294	AE003421
10	23	3.2	729	HSA328489
11	23	3.2	6234	AX346523
12	23	3.2	14535	AF442957
13	23	3.2	14536	AF467260
14	23	3.2	135772	AC122478
15	23	3.2	166478	AC105750
16	23	3.2	180760	AC131665
17	23	3.2	209969	AC102396
18	23	3.2	223156	AC111742
19	23	3.2	246528	AC128573
20	22	3.1	6075	AX346452
21	22	3.1	142569	AC133381
22	22	3.1	152323	AL954183
23	22	3.1	158581	AC147528
24	22	3.1	162451	AL353597
25	22	3.1	171708	AC067956
26	22	3.1	175436	BX663508
27	22	3.1	177101	AC146642
28	22	3.1	178937	BX511195
29	22	3.1	181803	BX248503
30	22	3.1	202098	BX470244
31	22	3.1	202495	CNS01DW6
32	22	3.1	202496	CNS01DW6
33	22	3.1	217707	BX248129

34	c	34	22	3.1 225702	2	AC121687	AC121687 Rattus no	c	90	21	2.9 198750	8	ATCHR1V85	AL161589 Arabidops
35	c	35	22	3.1 230766	2	AC113698	AC113698 Rattus no	c	91	21	2.9 199362	2	AC145945	AC145945 Gallus
36	c	36	22	3.1 231383	5	AL844512	AL844512 Zebrafish	c	92	21	2.9 201128	2	AC111034	AC111034 Mus muscu
37	c	37	22	3.1 234724	10	AL683894	AL683894 Mouse DNA	c	93	21	2.9 202060	10	AC122250	AC122250 Mus muscu
38	c	38	22	3.1 244650	2	AC106532	AC106532 Rattus no	c	94	21	2.9 203257	10	AL596450	AL596450 Mouse DNA
39	c	39	22	3.1 248546	2	AC136590	AC136590 Rattus no	c	95	21	2.9 220487	2	AC094211	AC094211 Rattus no
40	c	40	22	3.1 251720	2	AC094479	AC094479 Rattus no	c	96	21	2.9 228065	2	AC146508	AC146508 Pan trogl
41	c	41	22	3.1 253798	2	AC129701	AC129701 Rattus no	c	97	21	2.9 229682	2	AC098363	AC098363 Rattus no
42	c	42	22	3.1 256945	2	AC097423	AC097423 Rattus no	c	98	21	2.9 238780	2	AC106635	AC106635 Rattus no
43	c	43	22	3.1 260277	2	AC114063	AC114063 Rattus no	c	99	21	2.9 247150	2	AC135416	AC135416 Medicago
44	c	44	22	3.1 274382	2	AC115329	AC115329 Rattus no	c	100	21	2.9 249002	2	BX649347	BX649347 Dantio rer
45	c	45	21	2.9 1207	3	ENHACTIN	M19871 E. histolyti	c	101	21	2.9 254524	2	AC095780	AC095780 Rattus no
46	c	46	21	2.9 2000	6	AX509503	AX509503 Sequence	c	102	21	2.9 254609	2	AC097153	AC097153 Rattus no
47	c	47	21	2.9 3510	3	U64538	U64538 Drosophila	c	103	21	2.9 273447	2	AC123481	AC123481 Rattus no
48	c	48	21	2.9 5156	6	AR085703	AR085703 Sequence	c	104	21	2.9 301136	3	AE003391	AE003391 Drosophila
49	c	49	21	2.9 5156	6	AR260569	AR260569 Sequence	c	105	21	2.9 331039	3	AC116968	AC116968 Dictyoste
50	c	50	21	2.9 5156	6	AR390840	AR390840 Sequence	c	106	21	2.9 349980	6	AX144572	AX144572 Sequence
51	c	51	21	2.9 6050	6	AX346913	AX346913 Sequence	c	107	20	2.8 134	3	AY145067	AY145067 Drosophila
52	c	52	21	2.9 8760	8	AF068574	AF068574 Arabidops	c	108	20	2.8 243	11	G74593	G74593 STS-283 Sm
53	c	53	21	2.9 18544	2	AC020199	AC020199 Drosophila	c	109	20	2.8 552	6	AX477761	AX477761 Sequence
54	c	54	21	2.9 28756	3	CFE2785	Z48582 Caenorhabdi	c	110	20	2.8 632	8	AF318995	AF318995 Postelsia
55	c	55	21	2.9 43159	8	AF193903	AF193903 Cafeteria	c	111	20	2.8 709	9	HS438128	AJ338128 Homo sapi
56	c	56	21	2.9 65811	9	AL451145	AL451145 Human DNA	c	112	20	2.8 1325	3	AF072442	AF072442 Plasmodiu
57	c	57	21	2.9 88270	8	AP004875	AP004875 Oryza sat	c	113	20	2.8 1409	6	AX509286	AX509286 Sequence
58	c	58	21	2.9 94695	8	ATF23E13	ATF23E13 Arabidops	c	114	20	2.8 1663	8	BT002936	BT002936 Arabidops
59	c	59	21	2.9 101901	8	AP003377	AP003377 Oryza sat	c	115	20	2.8 2232	8	SCNAP4	X16727 Yeast HAP4
60	c	60	21	2.9 116635	2	AC147537	AC147537 Medicago	c	116	20	2.8 2412	1	AF325895	AF325895 Stephyloc
61	c	61	21	2.9 120380	2	AC147482	AC147482 Medicago	c	117	20	2.8 2636	8	AF203584	AF203584 Zornila sp
62	c	62	21	2.9 138989	2	AC027186	AC027186 Homo sapi	c	118	20	2.8 3427	8	SCYRL10C	228110 S. cerevisia
63	c	63	21	2.9 143538	2	AC026555	AC026555 Homo sapi	c	119	20	2.8 3604	6	BD193886	BD193886 Enterococ
64	c	64	21	2.9 146705	2	AC007971	AC007971 Homo sapi	c	120	20	2.8 4261	8	SCMGMDNA	X62834 S. cerevisia
65	c	65	21	2.9 147246	2	AP003538	AP003538 Oryza sat	c	121	20	2.8 4377	8	SCYOR211C	275119 S. cerevisia
66	c	66	21	2.9 150900	2	AC068075	AC068075 Homo sapi	c	122	20	2.8 4500	5	SSGNRH	X74957 S. salar sgm
67	c	67	21	2.9 152451	9	AC028674	AC028674 Homo sapi	c	123	20	2.8 4545	8	SCYRL10W	228109 S. cerevisia
68	c	68	21	2.9 155001	2	AC013827	AC013827 Homo sapi	c	124	20	2.8 4615	8	YSCDYN1PA	L07419 Saccharomyc
69	c	69	21	2.9 156527	9	AL161439	AL161439 Human DNA	c	125	20	2.8 5318	8	SCYOR212W	275120 S. cerevisia
70	c	70	21	2.9 159193	2	AP004792	AP004792 Oryza sat	c	126	20	2.8 6067	6	AX279988	AX279988 Sequence
71	c	71	21	2.9 163623	9	AC005203	AC005203 Homo sapi	c	127	20	2.8 6067	6	AX346087	AX346087 Sequence
72	c	72	21	2.9 163981	9	AC009647	AC009647 Homo sapi	c	128	20	2.8 6067	6	AX34608	AX34608 Sequence
73	c	73	21	2.9 164943	9	AP005272	AP005272 Homo sapi	c	129	20	2.8 6134	6	AX346084	AX346084 Sequence
74	c	74	21	2.9 167350	2	AC129717	AC129717 Oryza sat	c	130	20	2.8 6548	8	SPPOLAL	X69673 Schistosach
75	c	75	21	2.9 167875	9	AL512506	AL512506 Human DNA	c	131	20	2.8 7187	6	AX344629	AX344629 Sequence
76	c	76	21	2.9 169663	9	AC146232	AC146232 Pan trogl	c	132	20	2.8 7203	6	AX346953	AX346953 Sequence
77	c	77	21	2.9 169702	2	AL356385	AL356385 Homo sapi	c	133	20	2.8 7631	6	AX345762	AX345762 Sequence
78	c	78	21	2.9 170560	2	BX648444	BX648444 Dantio rer	c	134	20	2.8 8883	6	AX251519	AX251519 Sequence
79	c	79	21	2.9 170583	2	AC068815	AC068815 Homo sapi	c	135	20	2.8 12356	6	AX251263	AX251263 Sequence
80	c	80	21	2.9 174739	9	AL356428	AL356428 Human DNA	c	136	20	2.8 15109	6	AB11192054	AB111923 Oryzalas 1
81	c	81	21	2.9 177727	10	AL732368	AL732368 Mouse DNA	c	137	20	2.8 15121	6	AR353926	AR353926 Sequence
82	c	82	21	2.9 178452	2	AC133925	AC133925 Oryza sat	c	138	20	2.8 15152	1	AE001171	AE001171 Sequence
83	c	83	21	2.9 178965	3	AC010117	AC010117 Drosophila	c	139	20	2.8 16823	1	AE000793	AE000793 Botreilia
84	c	84	21	2.9 184478	2	AC134322	AC134322 Medicago	c	140	20	2.8 16933	1	BBU43414	U43414 Botreilia bu
85	c	85	21	2.9 185095	6	AP003436	AP003436 Oryza sat	c	141	20	2.8 17626	2	AC014858	AC014858 Drosophila
86	c	86	21	2.9 185481	2	AC091088	AC091088 Oryza sat	c	142	20	2.8 18519	2	AC019781	AC019781 Drosophila
87	c	87	21	2.9 186044	2	AC023512	AC023512 Homo sapi	c	143	20	2.8 24900	3	AF016654	AF016654 Caenorhab
88	c	88	21	2.9 188350	2	AC016501	AC016501 Homo sapi	c	144	20	2.8 32415	9	AC013646	AC013646 Homo sapi
89	c	89	21	2.9 188557	1	BX246586	BX246586 Blochmann	c	145	20	2.8 32415	9	AC013646	AC013646 Homo sapi

146	c 146	2.8 32568	3	CEM02B8	281136 Caenorhabdit	c 203	2.8 131403	14	AF271059	AF271059 Helicover
c 147	c 147	2.8 32788	3	CEP33H1	Z68783 Caenorhabdit	204	2.8 131903	9	HS360E18	Z62203 Human DNA s
c 148	c 148	2.8 33173	8	SC33NB	X92441 S.cerevisia	205	2.8 133116	2	AC146631	AC146631 Medicago
c 149	c 149	2.8 33887	8	AL606828	AL606828 Human DNA	206	2.8 136374	2	AC142035	AC142035 Rattus no
c 150	c 150	2.8 34284	8	SPAC3H5	Z99286 S.pombe chr	207	2.8 136814	9	AC064826	AC064826 Homo sapi
c 151	c 151	2.8 35757	8	SCAPLAP	X71133 S.cerevisia	c 208	2.8 137911	2	AC009769	AC009769 Homo sapi
c 152	c 152	2.8 43090	3	CEC08B6	Z72502 Caenorhabdit	209	2.8 139843	2	AL158145	AL158145 Homo sapi
c 153	c 153	2.8 52872	9	AC117946	AC117946 Homo sapi	c 210	2.8 140385	9	HS20B11	AL031770 Human DNA
c 154	c 154	2.8 53721	2	AC013963	AC013963 Drosophila	211	2.8 142257	5	BX005151	BX005151 Zebrafish
c 155	c 155	2.8 60901	2	AL160406	AL160406 Human DNA	c 212	2.8 143669	9	AP006307	AP006307 Homo sapi
c 156	c 156	2.8 62104	2	AC024919	AC024919 Homo sapi	c 213	2.8 144286	2	AC108897	AC108897 Felis cat
c 157	c 157	2.8 64263	9	AC132660	AC132660 Homo sapi	214	2.8 144388	2	AC091433	AC091433 Homo sapi
c 158	c 158	2.8 69133	9	AL691458	AL691458 Human DNA	c 215	2.8 144841	9	AC108101	AC108101 Homo sapi
c 159	c 159	2.8 74749	2	AC137669	AC137669 Medicago	216	2.8 145019	2	AC053488	AC053488 Homo sapi
c 160	c 160	2.8 75001	8	AC093167	AC093167 Homo sapi	217	2.8 145926	2	AC021697	AC021697 Homo sapi
c 161	c 161	2.8 77350	8	ATT28B15	AL132972 Arabidops	218	2.8 146242	10	AC122539	AC122539 Mus muscu
c 162	c 162	2.8 81092	2	AC021397	AC021397 Homo sapi	219	2.8 147803	9	ALJ36867	ALJ36867 Human DNA
c 163	c 163	2.8 85735	9	AC069336	AC069336 Homo sapi	c 220	2.8 148286	5	BX470246	BX470246 Zebrafish
c 164	c 164	2.8 87770	8	AP003907	AP003907 Oryza sat	c 221	2.8 148678	5	AL929281	AL929281 Zebrafish
c 165	c 165	2.8 88643	8	AC022522	AC022522 Arabidops	c 222	2.8 148720	2	AC019353	AC019353 Homo sapi
c 166	c 166	2.8 91516	9	AL731577	AL731577 Human DNA	c 223	2.8 148870	9	HS173A13	AL035688 Human DNA
c 167	c 167	2.8 92900	8	AP003825	AP003825 Oryza sat	224	2.8 149335	2	AC009651	AC009651 Homo sapi
c 168	c 168	2.8 95739	2	AP004644	AP004644 Oryza sat	c 225	2.8 152019	2	BX663494	BX663494 Homo sapi
c 169	c 169	2.8 98902	9	HS128N22	Z97629 Human DNA	c 226	2.8 152306	9	AC113617	AC113617 Homo sapi
c 170	c 170	2.8 101502	9	AC092280	AC092280 Homo sapi	c 227	2.8 152553	9	CNS010XE	AL139285 Human chr
c 171	c 171	2.8 102029	9	AC133537	AC133537 Homo sapi	c 228	2.8 152607	2	AC107321	AC107321 Felis cat
c 172	c 172	2.8 106627	5	ALJ592202	ALJ592202 Zebrafish	c 229	2.8 153571	1	AF454824	AF454824 Enterococ
c 173	c 173	2.8 108100	9	AC103881	AC103881 Homo sapi	230	2.8 153867	10	AC122501	AC122501 Mus muscu
c 174	c 174	2.8 110000	2	AC094933_0	AC094933 Rattus no	231	2.8 153941	2	BX322575	BX322575 Human DNA
c 175	c 175	2.8 110000	2	AC097394_1	Continuation (2 of	c 232	2.8 154918	9	HSJ267A8	AL121957 Human DNA
c 176	c 176	2.8 110000	2	AC097394_2	Continuation (3 of	c 233	2.8 154924	4	AC132153	AC132153 Homo sapi
c 177	c 177	2.8 110000	2	AC06120_2	Continuation (19 o	c 234	2.8 155680	2	AC120887	AC120887 Oryza sat
c 178	c 178	2.8 110000	2	AC115281_1	Continuation (2 of	c 235	2.8 156978	2	AC023379	AC023379 Homo sapi
c 179	c 179	2.8 110000	2	AC120430_0	AC120430 Mus muscu	236	2.8 157270	9	AF236874	AF236874 Homo sapi
c 180	c 180	2.8 110000	2	AC120922_2	Continuation (3 of	237	2.8 157561	3	AC099309	AC099309 Drosophila
c 181	c 181	2.8 110000	2	BX546456_1	Continuation (2 of	c 238	2.8 157743	2	AC140898	AC140898 Homo sapi
c 182	c 182	2.8 110000	2	PPMAL13_18	Continuation (19 o	239	2.8 158019	8	CNS08CAU	AL844497 Oryza sat
c 183	c 183	2.8 110000	3	AC116957_0	AC116957 Dictyoste	240	2.8 158666	2	AC140420	AC140420 Mus muscu
c 184	c 184	2.8 110000	9	AE014305_4	Continuation (5 of	c 241	2.8 158770	2	AC147467	AC147467 Homo sapi
c 185	c 185	2.8 110879	2	AC138795_1	AC138795 Homo sapi	c 242	2.8 158710	9	ALJ360020	ALJ360020 Human DNA
c 186	c 186	2.8 114218	2	AC146536	AC146536 Daeypus n	243	2.8 159593	2	AC007924	AC007924 Homo sapi
c 187	c 187	2.8 115224	9	ALJ359539	ALJ359539 Human DNA	244	2.8 160762	9	AP000475	AP000475 Homo sapi
c 188	c 188	2.8 116557	9	AC107022	AC107022 Homo sapi	245	2.8 161826	9	ALJ38532	ALJ38532 Human DNA
c 189	c 189	2.8 116871	2	ALJ38738	ALJ38738 Homo sapi	246	2.8 162575	9	ALJ57829	ALJ57829 Human DNA
c 190	c 190	2.8 117166	2	AC146366	AC146366 Daeypus n	247	2.8 163040	2	AC126240	AC126240 Felis cat
c 191	c 191	2.8 117434	9	HSJ0565P6	AL049742 Human DNA	248	2.8 163246	9	AC010196	AC010196 Homo sapi
c 192	c 192	2.8 118374	8	AC025416	AC025416 Genomlac s	249	2.8 163443	5	ALJ773542	ALJ773542 Zebrafish
c 193	c 193	2.8 121675	2	AC144645	AC144645 Medicago	c 250	2.8 163604	9	AP006301	AP006301 Homo sapi
c 194	c 194	2.8 122241	2	AP004129	AP004129 Oryza sat	251	2.8 164690	2	AC016846	AC016846 Homo sapi
c 195	c 195	2.8 123576	9	AC015969	AC015969 Homo sapi	c 252	2.8 165152	9	ALJ589669	ALJ589669 Human DNA
c 196	c 196	2.8 124096	9	AC005247	AC005247 Homo sapi	c 253	2.8 165154	2	ALJ41858	ALJ41858 Sus scrofa
c 197	c 197	2.8 124169	2	AC146752	AC146752 Medicago	c 254	2.8 165773	9	ALJ57037	ALJ57037 Human DNA
c 198	c 198	2.8 125238	9	AC008842	AC008842 Homo sapi	255	2.8 165870	9	AC025089	AC025089 Homo sapi
c 199	c 199	2.8 127292	2	BX465836	BX465836 Danio rer	c 256	2.8 166156	5	BX649398	BX649398 Zebrafish
c 200	c 200	2.8 128525	8	AP003118	AP003118 Oryza sat	c 257	2.8 166349	2	AC013707	AC013707 Homo sapi
c 201	c 201	2.8 130760	14	AF303045	AF303045 Helicover	c 258	2.8 166349	2	AC013707	AC013707 Homo sapi
c 202	c 202	2.8 130869	14	AF334030	AF334030 Helicover	c 259	2.8 166452	9	AC090453	AC090453 Homo sapi

260	2.8	166860	2	BX323866	Danio rer	317	2.8	183540	10	AC084416	AC084416 Mus muscu
261	2.8	167912	3	AC007650	Drosophila	318	2.8	186030	8	CNS08CTW	AL731747 Oryza sat
262	2.8	166186	2	AC117385	AC117385 Homo sapi	319	2.8	188057	2	AC023923	AC023923 Homo sapi
263	2.8	166518	2	BX548172	Danio rer	320	2.8	188283	2	AC113661	AC113661 Rattus no
264	2.8	166909	9	AC010165	Homo sapi	321	2.8	188524	2	AC123754	AC123754 Mus muscu
265	2.8	165288	9	AL583853	Human DNA	322	2.8	188713	2	AC128580	AC128580 Rattus no
266	2.8	169530	5	BX004756	BX004756 Zebrafish	323	2.8	189286	9	AC093906	AC093906 Homo sapi
267	2.8	169689	2	BX323459	Danio rer	324	2.8	191815	2	AL955334	AL955334 Danio rer
268	2.8	170095	9	AL356131	Human DNA	325	2.8	192550	2	AC026103	AC026103 Homo sapi
269	2.8	170543	9	AC021012	Homo sapi	326	2.8	192563	9	AL354763	AL354763 Human DNA
270	2.8	170544	9	CNS05TCC	AL355093 Human chr	327	2.8	193803	9	AC022819	AC022819 Homo sapi
271	2.8	170630	2	AC034163	AC034163 Homo sapi	328	2.8	194672	2	BX890620	BX890620 Danio rer
272	2.8	170862	2	AC087784	AC087784 Homo sapi	329	2.8	194717	9	AC113424	AC113424 Homo sapi
273	2.8	171068	5	AL356241	Human DNA	330	2.8	194979	3	AC091209	AC091209 Drosophila
274	2.8	171078	5	AL845301	AL845301 Zebrafish	331	2.8	195660	2	BX649568	BX649568 Danio rer
275	2.8	171081	2	AC023402	AC023402 Homo sapi	332	2.8	196604	2	AL627100	AL627100 Homo sapi
276	2.8	171135	9	AC093895	AC093895 Homo sapi	333	2.8	196604	2	AL627100	AL627100 Homo sapi
277	2.8	171141	5	AL844196	AL844196 Zebrafish	334	2.8	196664	2	AC106628	AC106628 Rattus no
278	2.8	171559	10	AL611982	AL611982 Mouse DNA	335	2.8	197346	9	AC008039	AC008039 Homo sapi
279	2.8	171632	9	AC110760	AC110760 Homo sapi	336	2.8	197684	2	BX323543	BX323543 Danio rer
280	2.8	172180	9	AC109494	AC109494 Homo sapi	337	2.8	198448	10	AC115118	AC115118 Mus muscu
281	2.8	172190	3	AC010668	AC010668 Drosophila	338	2.8	198412	10	AC122342	AC122342 Mus muscu
282	2.8	172324	2	AC111345	AC111345 Rattus no	339	2.8	199342	2	AC129961	AC129961 Mus muscu
283	2.8	172540	3	AC010071	AC010071 Drosophila	340	2.8	199601	2	AC135240	AC135240 Mus muscu
284	2.8	172558	9	AC023509	AC023509 Homo sapi	341	2.8	199646	10	AC122264	AC122264 Mus muscu
285	2.8	172834	2	AC011277	AC011277 Homo sapi	342	2.8	199894	2	BX247872	BX247872 Danio rer
286	2.8	172898	9	AL929288	AL929288 Human DNA	343	2.8	199896	2	AC127812	AC127812 Rattus no
287	2.8	173631	2	AC016897	AC016897 Homo sapi	344	2.8	200562	5	AL929016	AL929016 Zebrafish
288	2.8	173845	9	AC018662	AC018662 Human chr	345	2.8	202848	2	AC113503	AC113503 Mus muscu
289	2.8	173853	2	AC018999	AC018999 Homo sapi	346	2.8	202911	2	AC119063	AC119063 Pan trogl
290	2.8	174012	5	AL929503	AL929503 Zebrafish	347	2.8	203128	10	AL732965	AL732965 Mouse DNA
291	2.8	174028	2	AC067831	AC067831 Homo sapi	348	2.8	203574	2	AC117660	AC117660 Mus muscu
292	2.8	174622	5	BX005044	BX005044 Zebrafish	349	2.8	204303	2	AC123111	AC123111 Rattus no
293	2.8	175010	3	BX682557	BX682557 Danio rer	350	2.8	204498	5	AL831791	AL831791 Zebrafish
294	2.8	175192	3	AC010576	AC010576 Drosophila	351	2.8	204539	5	AL934843	AL934843 Zebrafish
295	2.8	175681	2	AC053486	AC053486 Homo sapi	352	2.8	204702	9	AL356937	AL356937 Human DNA
296	2.8	176621	2	BX530089	BX530089 Danio rer	353	2.8	205202	2	AC139347	AC139347 Mus muscu
297	2.8	176275	2	AC025551	AC025551 Homo sapi	354	2.8	205855	2	AC128519	AC128519 Rattus no
298	2.8	176366	2	AC118779	AC118779 Mus muscu	355	2.8	206960	2	AC128121	AC128121 Rattus no
299	2.8	176432	2	AC130794	AC130794 Felis cat	356	2.8	206982	2	BX510641	BX510641 Danio rer
300	2.8	176921	9	AC016080	AC016080 Homo sapi	357	2.8	207256	10	AL669950	AL669950 Mouse DNA
301	2.8	177087	10	AL672293	AL672293 Mouse DNA	358	2.8	207622	2	BX323531	BX323531 Danio rer
302	2.8	177761	9	AC037479	AC037479 Homo sapi	359	2.8	208168	2	BX664618	BX664618 Danio rer
303	2.8	178148	5	BX005011	BX005011 Zebrafish	360	2.8	208219	2	AC120689	AC120689 Rattus no
304	2.8	178281	2	AC118622	AC118622 Mus muscu	361	2.8	209697	2	AC123632	AC123632 Mus muscu
305	2.8	178491	2	BX005174	BX005174 Danio rer	362	2.8	211463	2	AC073499	AC073499 Homo sapi
306	2.8	178495	2	BX510329	BX510329 Danio rer	363	2.8	212482	14	AF303741	AF303741 Chilio liri
307	2.8	178610	10	AC105951	AC105951 Mus muscu	364	2.8	212724	2	AC140962	AC140962 Mus muscu
308	2.8	179202	2	AC025935	AC025935 Homo sapi	365	2.8	215464	2	BX572645	BX572645 Danio rer
309	2.8	179777	2	AC067879	AC067879 Homo sapi	366	2.8	215651	2	AC132634	AC132634 Rattus no
310	2.8	180389	9	AC063944	AC063944 Homo sapi	367	2.8	215848	2	BX323876	BX323876 Danio rer
311	2.8	180650	9	AC109474	AC109474 Homo sapi	368	2.8	216143	3	AC084197	AC084197 Caenorhab
312	2.8	181419	9	AL445984	AL445984 Human DNA	369	2.8	216152	2	AC101858	AC101858 Mus muscu
313	2.8	181443	9	AC099786	AC099786 Homo sapi	370	2.8	217462	2	AC137222	AC137222 Rattus no
314	2.8	182018	2	AC015464	AC015464 Homo sapi	371	2.8	217616	2	AC079531	AC079531 Mus muscu
315	2.8	182020	9	AC113170	AC113170 Homo sapi	372	2.8	219283	2	AC108550	AC108550 Rattus no
316	2.8	182061	2	AC102217	AC102217 Mus muscu	373	2.8	220157	2	AC105462	AC105462 Rattus no

374	20	2.8 220715	9	AC012410	AC012410 Homo sapi	c 431	20	2.8 348650	1	AP003364	AP003364 Staphyloc
375	20	2.8 221926	2	EX005245	EX005245 Dario rer	c 432	20	2.8 349980	6	AX345466	AX345466 Sequence
c 376	20	2.8 223728	2	AC097906	AC097906 Rattus no	c 433	19	2.7 285	1	AF358691	AF358691 Helicobac
377	20	2.8 227413	3	AE003702	AE003702 Drosophill	c 434	19	2.7 298	3	AF154730	AF154730 Megaseila
378	20	2.8 229799	2	AC097797	AC097797 Rattus no	c 435	19	2.7 342	3	AF126312	AF126312 Megaseila
c 379	20	2.8 230206	2	AC114140	AC114140 Rattus no	c 436	19	2.7 394	3	AF154728	AF154728 Megaseila
c 380	20	2.8 230841	2	AC103437	AC103437 Rattus no	c 437	19	2.7 504	5	AF325252	AF325252 Homblagru
381	20	2.8 231373	2	AC112543	AC112543 Rattus no	c 438	19	2.7 639	11	BN057815	BN057815 S21P6747
382	20	2.8 231919	2	AC111770	AC111770 Rattus no	c 439	19	2.7 671	6	AX685991	AX685991 Sequence
c 383	20	2.8 232834	10	ALB844167	ALB844167 Mouse DNA	c 440	19	2.7 820	11	BN058264	BN058264 S21P6542
384	20	2.8 234622	2	AC135834	AC135834 Rattus no	c 441	19	2.7 910	8	AY122437	AY122437 Forchham
c 385	20	2.8 235927	2	AC116577	AC116577 Mus muscu	c 442	19	2.7 938	8	AY122465	AY122465 Tovarila P
c 386	20	2.8 236261	2	AC123165	AC123165 Rattus no	c 443	19	2.7 975	10	AB037362S7	AB037362 Mus muscu
c 387	20	2.8 238577	10	AC095563	AC095563 Rattus no	c 444	19	2.7 1002	1	AF416986	AF416986 Pasteurel
388	20	2.8 238577	2	AC098281	AC098281 Rattus no	c 445	19	2.7 1220	6	AX429478	AX429478 Sequence
389	20	2.8 239069	2	AC108289	AC108289 Rattus no	c 446	19	2.7 1653	8	AP004501	AP004501 Rattus cor
c 390	20	2.8 239803	2	AC094312	AC094312 Rattus no	c 447	19	2.7 1653	10	AB016795	AB016795 Mus muscu
391	20	2.8 242308	2	AC103157	AC103157 Rattus no	c 448	19	2.7 1707	8	SPCARARG	SPCARARG Rattus no
392	20	2.8 243075	2	AC097827	AC097827 Rattus no	c 449	19	2.7 1720	3	AF153409	AF153409 Trypanoso
c 393	20	2.8 245090	2	EX090597	EX090597 Dario rer	c 450	19	2.7 1960	3	AY294149	AY294149 Verillillife
c 394	20	2.8 245581	10	AC133000	AC133000 Rattus No	c 451	19	2.7 2078	3	AC114238	AC114238 Dictyoste
c 395	20	2.8 245802	2	AC006279	AC006279 Plasmodiu	c 452	19	2.7 2226	3	MTDVTN	MTDVTN Dictyoste
396	20	2.8 247565	2	AC124873	AC124873 Rattus no	c 453	19	2.7 2291	6	AX429477	AX429477 Sequence
c 397	20	2.8 248917	2	AC111455	AC111455 Rattus no	c 454	19	2.7 2407	9	BC014416	BC014416 Homo sapi
c 398	20	2.8 250029	3	PFMAL3P7	PFMAL3P7 Plasmodiu	c 455	19	2.7 2558	10	BC063104	BC063104 Mus muscu
399	20	2.8 253305	3	AC096421	AC096421 Rattus no	c 456	19	2.7 2640	8	AP004924	AP004924 Rattus cor
400	20	2.8 253507	2	EX088547	EX088547 Zebrfish	c 457	19	2.7 2682	6	AR067691	AR067691 Sequence
c 401	20	2.8 256446	5	EX088547	EX088547 Zebrfish	c 458	19	2.7 2682	6	AR067691	AR067691 Sequence
c 402	20	2.8 256789	2	AC121054	AC121054 Rattus no	c 459	19	2.7 2682	6	AR067691	AR067691 Sequence
c 403	20	2.8 256867	2	AC109662	AC109662 Rattus no	c 460	19	2.7 2711	10	BC005616	BC005616 Homo sapien
c 404	20	2.8 258569	2	AC097908	AC097908 Rattus no	c 461	19	2.7 3039	8	AP006072	AP006072 Mus muscu
405	20	2.8 260929	3	AE014852	AE014852 Plasmodiu	c 462	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
406	20	2.8 262830	2	AC125306	AC125306 Rattus no	c 463	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
407	20	2.8 268409	2	AC130995	AC130995 Rattus no	c 464	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 408	20	2.8 270733	2	AC128455	AC128455 Rattus no	c 465	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 409	20	2.8 271827	2	AC125062	AC125062 Mus muscu	c 466	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 410	20	2.8 272071	2	AC109111	AC109111 Rattus no	c 467	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
411	20	2.8 273331	2	AC110676	AC110676 Rattus no	c 468	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
412	20	2.8 276815	2	AC109098	AC109098 Rattus no	c 469	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 413	20	2.8 279131	2	AC122614	AC122614 Rattus no	c 470	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 414	20	2.8 291061	2	AC099169	AC099169 Rattus no	c 471	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
415	20	2.8 293875	2	AE003532	AE003532 Drosophill	c 472	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 416	20	2.8 299308	2	AC006898	AC006898 Caenorhab	c 473	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
417	20	2.8 299859	2	AC128993	AC128993 Rattus no	c 474	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 418	20	2.8 299932	2	AC129722	AC129722 Rattus no	c 475	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
419	20	2.8 302363	1	AE016948	AE016948 Enterococ	c 476	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 420	20	2.8 304050	1	AP004829	AP004829 Staphyloc	c 477	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
421	20	2.8 307717	2	AC108630	AC108630 Rattus no	c 478	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 422	20	2.8 307750	1	AP003136	AP003136 Staphyloc	c 479	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 423	20	2.8 308092	3	AY333070	AY333070 Drosophill	c 480	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
424	20	2.8 312488	10	AC139934	AC139934 Mus muscu	c 481	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 425	20	2.8 313573	3	CEX57G11C	CEX57G11C Rattus no	c 482	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 426	20	2.8 314421	2	AC110404	AC110404 Rattus no	c 483	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 427	20	2.8 328561	2	AE003843	AE003843 Drosophill	c 484	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
428	20	2.8 340000	9	HS21C027	HS21C027 Homo sapi	c 485	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
429	20	2.8 348600	1	AB063521	AB063521 Wt9913swo	c 486	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste
c 430	20	2.8 348600	1	AB063521	AB063521 Wt9913swo	c 487	19	2.7 3182	3	DDIMRO3	DDIMRO3 Dictyoste

488	19	2.7	7321	6	AX252038	AX252038	Sequence	545	19	2.7	39553	3	CEJCH	282274 Caenorhabd.
489	19	2.7	7321	6	AX344420	AX344420	Sequence	546	19	2.7	39915	9	AC010512	AC010512 Homo sapi
490	19	2.7	7321	6	AX346817	AX346817	Sequence	547	19	2.7	40102	9	AC010647	AC010647 Homo sapi
491	19	2.7	7776	3	U70846	U70846	Caenorhabd.	548	19	2.7	40392	3	U21308	U21308 Caenorhabd.
492	19	2.7	7922	6	AX344678	AX344678	Sequence	549	19	2.7	41598	9	HS16M16	AL035532 Homo sapi
493	19	2.7	8196	6	AX281427	AX281427	Sequence	550	19	2.7	41628	3	U39994	U39994 Caenorhabd.
494	19	2.7	8196	6	AX345994	AX345994	Sequence	551	19	2.7	41628	3	U39994	U39994 Caenorhabd.
495	19	2.7	8196	6	AX346893	AX346893	Sequence	552	19	2.7	43311	2	HSN3F10	299131 Homo sapi
496	19	2.7	8201	6	AX345208	AX345208	Sequence	553	19	2.7	44726	3	U37429	U37429 Caenorhabd.
497	19	2.7	8201	6	AX346551	AX346551	Sequence	554	19	2.7	46024	2	AC100659	AC100659 Mus muscu
498	19	2.7	8234	6	AX346551	AX346551	Sequence	555	19	2.7	47577	3	AF366436	AF366436 Tetrahyme
499	19	2.7	8392	1	BATROPEA	BATROPEA	Sequence	556	19	2.7	47738	2	AC125417	AC125417 Homo sapi
500	19	2.7	9238	6	AX323752	AX323752	Sequence	557	19	2.7	48123	2	AC130288	AC130288 Homo sapi
501	19	2.7	9254	6	AX822423	AX822423	Sequence	558	19	2.7	53890	9	AL672310	AL672310 Homo sapi
502	19	2.7	9254	6	AX826063	AX826063	Sequence	559	19	2.7	54079	9	AC104172	AC104172 Homo sapi
503	19	2.7	10052	3	CEI13	CEI13	Caenorhabd.	560	19	2.7	54958	2	AC090760	AC090760 Homo sapi
504	19	2.7	11090	8	SPBP26C9	SPBP26C9	Sequence	561	19	2.7	55432	2	AC017613	AC017613 Drosophi1
505	19	2.7	11097	1	AE014103	AE014103	Buchnera	562	19	2.7	56283	2	AC020012	AC020012 Drosophi1
506	19	2.7	11729	6	AX345797	AX345797	Sequence	563	19	2.7	56954	2	BX510330	Continuation (4 of
507	19	2.7	11828	1	AE006118	AE006118	Pasteurel	564	19	2.7	59040	9	AC126170	AC126170 Homo sapi
508	19	2.7	12007	6	AX345619	AX345619	Sequence	565	19	2.7	59072	2	AC131930	AC131930 Homo sapi
509	19	2.7	12465	6	AX277868	AX277868	Sequence	566	19	2.7	60994	9	AL442647	AL442647 Human DNA
510	19	2.7	12465	6	AX345336	AX345336	Sequence	567	19	2.7	61082	8	NCB19C19	AL665992 Neurospor
511	19	2.7	14422	3	AF466146	AF466146	Mellipona	568	19	2.7	62978	2	AC100958	AC100958 Mus muscu
512	19	2.7	15674	6	AX281365	AX281365	Sequence	569	19	2.7	63288	2	AC011762	AC011762 Drosophi1
513	19	2.7	15674	6	AX345264	AX345264	Sequence	570	19	2.7	63421	2	AC137739	AC137739 Homo sapi
514	19	2.7	15674	6	AX348945	AX348945	Sequence	571	19	2.7	64707	3	AC115607	AC115607 Dictyoste
515	19	2.7	15767	6	AX281442	AX281442	Sequence	572	19	2.7	65107	2	AC079962	AC079962 Homo sapi
516	19	2.7	15767	6	AX346109	AX346109	Sequence	573	19	2.7	65333	2	AC103832	AC103832 Homo sapi
517	19	2.7	17461	3	U23180	U23180	Caenorhabd.	574	19	2.7	68421	5	BX005423	BX005423 Zebrafish
518	19	2.7	18218	6	AX346850	AX346850	Sequence	575	19	2.7	68550	2	AC118389	Continuation (6 of
519	19	2.7	18624	6	AX346604	AX346604	Sequence	576	19	2.7	68801	9	AP003399	AP003399 Homo sapi
520	19	2.7	22012	2	AC014468	AC014468	Drosophi1	577	19	2.7	69362	9	AL451132	AL451132 Human DNA
521	19	2.7	22881	10	AF287142	AF287142	Mus muscu	578	19	2.7	70000	8	AP003848	AP003848 Oryza sat
522	19	2.7	23024	6	AX089494	AX089494	Sequence	579	19	2.7	70043	9	AL157776	AL157776 Human DNA
523	19	2.7	24071	8	AP006406	AP006406	Lotus cor	580	19	2.7	70511	2	AC091083	AC091083 Homo sapi
524	19	2.7	24707	3	CEFI4E5	CEFI4E5	Caenorhabd.	581	19	2.7	71482	2	HSN5688	299132 Homo sapi
525	19	2.7	25833	3	CEC0284	CEC0284	Caenorhabd.	582	19	2.7	71971	9	BX293535	BX293535 Human DNA
526	19	2.7	26344	9	AC096671	AC096671	Homo sapi	583	19	2.7	72440	2	AC113794	Continuation (6 of
527	19	2.7	26435	3	U00034	U00034	Caenorhabd.	584	19	2.7	72631	5	AL929299	AL929299 Zebrafish
528	19	2.7	26855	2	AL3391984	AL3391984	Homo sapi	585	19	2.7	72735	8	AP004467	AP004467 Lotus cor
529	19	2.7	27271	3	CEC40H1	CEC40H1	Caenorhabd.	586	19	2.7	73053	2	AC100629	AC100629 Mus muscu
530	19	2.7	27454	10	AY215076	AY215076	Mus muscu	587	19	2.7	73635	2	AC100591	AC100591 Mus muscu
531	19	2.7	28105	3	U41011	U41011	Caenorhabd.	588	19	2.7	75531	3	AC005111	AC005111 Drosophi1
532	19	2.7	31048	3	U80447	U80447	Caenorhabd.	589	19	2.7	76568	3	MBREV	AF538053 Monosiga
533	19	2.7	33270	3	AE016439	AE016439	Caenorhabd.	590	19	2.7	78293	9	AC004636	AC004636 Homo sapi
534	19	2.7	34000	3	U28992	U28992	Drosophi1	591	19	2.7	79426	10	AL807830	AL807830 Mouse DNA
535	19	2.7	35003	2	AC020194	AC020194	Drosophi1	592	19	2.7	79652	6	AX711882	AX711882 Sequence
536	19	2.7	36261	3	U41535	U41535	Caenorhabd.	593	19	2.7	79743	9	AL451064	AL451064 Human DNA
537	19	2.7	36411	9	AC016626	AC016626	Homo sapi	594	19	2.7	81427	9	AC078960	AC078960 Homo sapi
538	19	2.7	36893	9	AC138034	AC138034	Homo sapi	595	19	2.7	82182	2	BX571840	BX571840 Dancio for
539	19	2.7	37036	9	HSN12086	HSN12086	Human DNA	596	19	2.7	82601	9	AL136971	AL136971 Human DNA
540	19	2.7	37640	9	AC003605	AC003605	Homo sapi	597	19	2.7	82652	8	AP006423	AP006423 Lotus cor
541	19	2.7	38289	1	AE000787	AE000787	Borrelia	598	19	2.7	83280	9	AP005638	AP005638 Homo sapi
542	19	2.7	38954	9	AC138033	AC138033	Homo sapi	599	19	2.7	83825	2	AC112729	AC112729 Drosophi1
543	19	2.7	39220	3	CEI12A7	CEI12A7	Caenorhabd.	600	19	2.7	83921	2	AC023848	AC023848 Homo sapi
544	19	2.7	39220	3	CEI12A7	CEI12A7	Caenorhabd.	601	19	2.7	83921	2	AC023848	AC023848 Homo sapi

602	19	2.7	84166	9	AC009095	AC009095 Homo sapi	c 659	19	2.7	110000	2	AC125589_1	Continuation (2 of
603	19	2.7	84250	10	AF481349	AF481349 Mus muscu	660	19	2.7	110000	2	AC129939_2	Continuation (3 of
604	19	2.7	85518	3	AC005449	AC005449 Drosophi	661	19	2.7	110000	2	AC130446_2	Continuation (3 of
605	19	2.7	85638	9	AC108126	AC108126 Homo sapi	662	19	2.7	110000	2	AC140127_1	Continuation (2 of
606	19	2.7	85902	2	AC127532	AC127532 Homo sapi	663	19	2.7	110000	2	AC140833_3	Continuation (4 of
607	19	2.7	86519	9	AC112242	AC112242 Homo sapi	664	19	2.7	110000	2	AC145943_1	Continuation (12 of
608	19	2.7	86701	9	AL353654	AL353654 Human DNA	665	19	2.7	110000	2	AC145944_1	Continuation (2 of
609	19	2.7	88900	2	AC020204	AC020204 Drosophi	666	19	2.7	110000	2	BX510330_2	Continuation (13 of
610	19	2.7	88982	5	AL732598	AL732598 Zebrafish	667	19	2.7	110000	2	FPMA18P1_12	Continuation (13 of
611	19	2.7	89677	9	AL732598	AL732598 Human DNA	668	19	2.7	110000	10	AY36310252_2	Continuation (13 of
612	19	2.7	89850	8	AC147365	AC147365 Medicago	669	19	2.7	110293	9	HSJD7686N3	Continuation (3 of
613	19	2.7	90531	8	AT75M18	AL025268 Arabidops	670	19	2.7	110892	2	AP004678	AP004678 Oryza sat
614	19	2.7	91825	2	AC019854	AC019854 Arabidops	671	19	2.7	111178	2	AP0020018	AC020018 Drosophi
615	19	2.7	92029	2	AL357492	AL357492 Homo sapi	672	19	2.7	111664	9	AL591499	AL591499 Human DNA
616	19	2.7	92053	2	AC012720	AC012720 Drosophi	673	19	2.7	113217	2	AC141110	AC141110 Medicago
617	19	2.7	92407	6	AB408757	AB408757 Sequence	674	19	2.7	113316	2	AC007866	AC007866 Trypanoso
618	19	2.7	92407	6	AB408757	AB408757 Sequence	675	19	2.7	113584	2	AC092411	AC092411 Felis cat
619	19	2.7	93321	9	BX649379	BX649379 Human DNA	676	19	2.7	113762	9	AC005294	AC005294 Homo sapi
620	19	2.7	94158	2	AC119619	AC119619 Homo sapi	677	19	2.7	114113	2	AL160005	AL160005 Homo sapi
621	19	2.7	95548	2	AC128940_3	Continuation (4 of	678	19	2.7	114340	9	AL358232	AL358232 Human DNA
622	19	2.7	96041	9	AC112643	AC112643 Homo sapi	679	19	2.7	114722	9	AC105758	AC105758 Homo sapi
623	19	2.7	96041	9	AC112643	AC112643 Homo sapi	680	19	2.7	115828	9	AL356458	AL356458 Human DNA
624	19	2.7	96623	2	AC108370	AC108370 Pan trogl	681	19	2.7	116098	2	AC023867	AC023867 Homo sapi
625	19	2.7	97391	9	AC010218	AC010218 Homo sapi	682	19	2.7	116540	10	AL954348	AL954348 Mouse DNA
626	19	2.7	97789	2	AL3590113	AL3590113 Human DNA	683	19	2.7	116576	9	AL356971	AL356971 Human DNA
627	19	2.7	98340	2	AC138012	AC138012 Medicago	684	19	2.7	116806	9	AL512643	AL512643 Human DNA
628	19	2.7	98340	2	AL353716	AL353716 Human DNA	685	19	2.7	117273	9	AL451138	AL451138 Human DNA
629	19	2.7	98454	2	AL592068	AL592068 Homo sapi	686	19	2.7	118705	8	AC126009	AC126009 Medicago
630	19	2.7	98595	9	AB001329	AB001329 Homo sapi	687	19	2.7	118763	9	AC114484	AC114484 Homo sapi
631	19	2.7	98899	2	AC107170_3	Continuation (4 of	688	19	2.7	119024	9	AL159987	AL159987 Human DNA
632	19	2.7	100132	9	AC092177	AC092177 Homo sapi	689	19	2.7	119450	14	U97553	U97553 Murine hepr
633	19	2.7	100272	9	HSDB42G6	AL109657 Human DNA	690	19	2.7	119550	14	AF105037	AF105037 Murine hepr
634	19	2.7	102784	2	AC104708	AC104708 Oryza sat	691	19	2.7	119853	9	AL136374	AL136374 Human DNA
635	19	2.7	103408	2	AL606524	AL606524 Homo sapi	692	19	2.7	119909	2	AC068935	AC068935 Homo sapi
636	19	2.7	104184	2	BX470110_5	Continuation (6 of	693	19	2.7	120000	9	AC004842	AC004842 Homo sapi
637	19	2.7	104186	5	BX088536	BX088536 Zebrafish	694	19	2.7	120035	8	AC123596	AC123596 Medicago
638	19	2.7	105239	9	AL390959	AL390959 Human DNA	695	19	2.7	120139	9	AC131281	AC131281 Homo sapi
639	19	2.7	105263	2	AC130652	AC130652 Medicago	696	19	2.7	120194	2	AL355474	AL355474 Human DNA
640	19	2.7	105297	2	AC140031	AC140031 Medicago	697	19	2.7	120668	2	AC139379	AC139379 Mus muscu
641	19	2.7	105682	3	AC116957_3	Continuation (4 of	698	19	2.7	121390	2	AC138985	AC138985 Homo sapi
642	19	2.7	106348	9	HSJ236116	AL049695 Human DNA	699	19	2.7	121533	2	AC124966	AC124966 Medicago
643	19	2.7	107011	8	AC138234	AC138234 Medicago	700	19	2.7	121533	2	AC124966	AC124966 Medicago
644	19	2.7	107097	8	AC005727	AC005727 Arabidops	701	19	2.7	121613	2	BX890615	BX890615 Dario rer
645	19	2.7	107710	8	AC144517	AC144517 Medicago	702	19	2.7	121664	9	AC114498	AC114498 Homo sapi
646	19	2.7	107967	2	AL353701	AL353701 Human DNA	703	19	2.7	121698	9	AC073578	AC073578 Homo sapi
647	19	2.7	108333	10	AL833783	AL833783 Mouse DNA	704	19	2.7	121820	2	AC135101	AC135101 Medicago
648	19	2.7	108821	2	AC138182	AC138182 Homo sapi	705	19	2.7	121820	2	AC135101	AC135101 Medicago
649	19	2.7	108847	8	AF002109	AF002109 Arabidops	706	19	2.7	122076	9	AC068051	AC068051 Homo sapi
650	19	2.7	109512	2	AC138251	AC138251 Mus muscu	707	19	2.7	122089	8	AC137552	AC137552 Medicago
651	19	2.7	109566	2	AL354830	AL354830 Mouse DNA	708	19	2.7	122948	9	HS891H21	AP004615 Oryza sat
652	19	2.7	109889	10	AL954830	Continuation (3 of	709	19	2.7	123201	2	AP004615	AL157936 Human DNA
653	19	2.7	110000	2	AC0978517_2	Continuation (3 of	710	19	2.7	124559	8	AL157936	AL157936 Human DNA
654	19	2.7	110000	2	AC094850_0	Continuation (10 o	711	19	2.7	124666	5	AC144759	AC144759 Zebrafish
655	19	2.7	110000	2	AC095863_09	Continuation (10 o	712	19	2.7	126287	5	BX255957	BX255957 Zebrafish
656	19	2.7	110000	2	AC096001_0	AC096001 Rattus no	713	19	2.7	127316	9	AL590239	AL590239 Human DNA
657	19	2.7	110000	2	AC107615_0	AC107615 Homo sapi	714	19	2.7	127340	9	AC129907	AC129907 Homo sapi
658	19	2.7	110000	2	AC118331_1	Continuation (2 of	715	19	2.7	127420	8	OSJN00281	AL731636 Oryza sat

716	19	2.7 127710	8	AC138452	AC138452	Medicago	773	19	2.7 145250	9	HSE24775	AL035534	Homo sapi
717	19	2.7 128024	9	AL1590455	AL1590455	Human DNA	774	19	2.7 145257	2	AC108178	AC108178	Felis cat
718	19	2.7 128374	9	AL1592347	AL1592347	Human DNA	775	19	2.7 146031	3	AE002665	AE002665	Drosophila
719	19	2.7 128358	9	AL1535623	AL1535623	Human DNA	776	19	2.7 146030	2	AC040943	AC040943	Homo sapi
720	19	2.7 128785	2	AC083877	AC083877	Homo sapi	777	19	2.7 147106	2	BX248521	BX248521	Danio rer
721	19	2.7 129779	9	AL1539457	AL1539457	Human DNA	778	19	2.7 147107	9	AC103849	AC103849	Homo sapi
722	19	2.7 129928	5	BX649355	BX649355	Zebrafish	779	19	2.7 147534	9	AC068620	AC068620	Homo sapi
723	19	2.7 130031	2	AC102685	AC102685	Mus muscu	780	19	2.7 147595	2	AC021778	AC021778	Homo sapi
724	19	2.7 130530	9	AT131217	AT131217	Homo sapi	781	19	2.7 147809	2	AC084362	AC084362	Homo sapi
725	19	2.7 130743	9	AC079772	AC079772	Homo sapi	782	19	2.7 148005	2	BX897667	BX897667	Danio rer
726	19	2.7 131005	5	AL929282	AL929282	Zebrafish	783	19	2.7 148289	5	AL845421	AL845421	Zebrafish
727	19	2.7 131680	2	AC146590	AC146590	Medicago	784	19	2.7 148337	2	AC021509	AC021509	Homo sapi
728	19	2.7 131736	2	AC021527	AC021527	Homo sapi	785	19	2.7 148396	9	AL157400	AL157400	Human DNA
729	19	2.7 132110	9	AP001610	AP001610	Homo sapi	786	19	2.7 148439	9	CNS01DX3	CNS01DX3	Human chr
730	19	2.7 132830	2	AP001865	AP001865	Homo sapi	787	19	2.7 148501	9	BX284929	BX284929	Human DNA
731	19	2.7 132882	2	AC132572	AC132572	Mus muscu	788	19	2.7 148504	2	AC138732	AC138732	Pongo pyg
732	19	2.7 133128	5	BX276083	BX276083	Zebrafish	789	19	2.7 148531	9	AC079089	AC079089	Homo sapi
733	19	2.7 133786	9	AC091839	AC091839	Homo sapi	790	19	2.7 148593	9	BS000073	BS000073	Pan trogl
734	19	2.7 134174	9	AC009495	AC009495	Homo sapi	791	19	2.7 148933	9	AC104232	AC104232	Homo sapi
735	19	2.7 134501	2	AC133231	AC133231	Rattus no	792	19	2.7 149353	8	OSJN00153	OSJN00153	Oryza sat
736	19	2.7 134614	9	BS000225	BS000225	Pan trogl	793	19	2.7 149440	2	AC112728	AC112728	Drosophila
737	19	2.7 135011	2	AC020183	AC020183	Drosophila	794	19	2.7 149502	10	AC130721	AC130721	Mus muscu
738	19	2.7 136960	9	AC092595	AC092595	Homo sapi	795	19	2.7 149549	9	AC099066	AC099066	Homo sapi
739	19	2.7 137229	9	AC010877	AC010877	Homo sapi	796	19	2.7 149727	2	AC073808	AC073808	Homo sapi
740	19	2.7 137857	9	AC122721	AC122721	Homo sapi	797	19	2.7 149803	2	BX322610	BX322610	Danio rer
741	19	2.7 138020	9	AC108043	AC108043	Homo sapi	798	19	2.7 149940	2	AC138560	AC138560	Lemur cat
742	19	2.7 138093	9	AL1606467	AL1606467	Human DNA	799	19	2.7 150067	2	BX323448	BX323448	Danio rer
743	19	2.7 138251	9	AC004908	AC004908	Homo sapi	800	19	2.7 150077	5	AL928881	AL928881	Zebrafish
744	19	2.7 138370	9	AL1354713	AL1354713	Human DNA	801	19	2.7 150172	9	AC034227	AC034227	Homo sapi
745	19	2.7 138500	2	AC118851	AC118851	Rattus no	802	19	2.7 150642	9	AC136309	AC136309	Homo sapi
746	19	2.7 138807	9	AL161650	AL161650	Human DNA	803	19	2.7 150899	2	AC018400	AC018400	Homo sapi
747	19	2.7 138929	2	AC011868	AC011868	Homo sapi	804	19	2.7 151012	9	AC079168	AC079168	Homo sapi
748	19	2.7 139394	2	AC010046	AC010046	Drosophila	805	19	2.7 151207	2	AP001031	AP001031	Homo sapi
749	19	2.7 139625	5	BX005458	BX005458	Zebrafish	806	19	2.7 151280	2	BX255888	BX255888	Danio rer
750	19	2.7 140094	9	HS2073	HS2073	Human DNA	807	19	2.7 151332	10	AC122298	AC122298	Mus muscu
751	19	2.7 140101	9	AC004648	AC004648	Homo sapi	808	19	2.7 151373	10	AC126551	AC126551	Mus muscu
752	19	2.7 140418	2	AC137822	AC137822	Medicago	809	19	2.7 151739	2	AC020691	AC020691	Homo sapi
753	19	2.7 141442	9	AL108471	AL108471	Homo sapi	810	19	2.7 152092	5	BX323067	BX323067	Zebrafish
754	19	2.7 141509	9	AC006044	AC006044	Homo sapi	811	19	2.7 152533	9	AC008483	AC008483	Homo sapi
755	19	2.7 141889	9	AC006334	AC006334	Homo sapi	812	19	2.7 152589	2	AC103906	AC103906	Carla fam
756	19	2.7 141913	9	AL1512452	AL1512452	Human DNA	813	19	2.7 152802	9	AC110274	AC110274	Homo sapi
757	19	2.7 142324	5	BX005420	BX005420	Zebrafish	814	19	2.7 152895	2	AC031979	AC031979	Homo sapi
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759	19	2.7 142665	9	HS202121	HS202121	Human DNA	816	19	2.7 153048	3	AC008362	AC008362	Drosophila
760	19	2.7 142895	2	BX323554	BX323554	Danio rer	817	19	2.7 153293	2	AC102064	AC102064	Mus muscu
761	19	2.7 143769	9	AC004914	AC004914	Homo sapi	818	19	2.7 153477	2	AC006278	AC006278	Plesmodiu
762	19	2.7 143770	9	AL1589987	AL1589987	Human DNA	819	19	2.7 153505	3	AC009849	AC009849	Drosophila
763	19	2.7 143890	9	HS662N3	HS662N3	Human DNA	820	19	2.7 153649	9	AL732372	AL732372	Human DNA
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765	19	2.7 144000	9	AC007621	AC007621	Homo sapi	822	19	2.7 154318	9	AC016720	AC016720	Homo sapi
766	19	2.7 144017	2	AC141685	AC141685	Apia meli	823	19	2.7 154429	2	AC090381	AC090381	Homo sapi
767	19	2.7 144107	2	AC010502	AC010502	Homo sapi	824	19	2.7 154519	9	BS000065	BS000065	Pan trogl
768	19	2.7 144233	2	AC068103	AC068103	Homo sapi	825	19	2.7 154685	9	AC007214	AC007214	Pan trogl
769	19	2.7 144406	2	AC008396	AC008396	Homo sapi	826	19	2.7 154779	3	AC092237	AC092237	Drosophila
770	19	2.7 144699	8	AP005451	AP005451	Oryza sat	827	19	2.7 154870	9	AC117461	AC117461	Homo sapi
771	19	2.7 144909	10	AL1590430	AL1590430	Mouse DNA	828	19	2.7 155040	9	AC145771	AC145771	Pan trogl
772	19	2.7 145201	9	AC084854	AC084854	Homo sapi	829	19	2.7 155318	9	HS791K14	HS791K14	Human DNA

c 830	19	2.7 155501	10	ALB44849	ALB44849 Mouse DNA	c 887	19	2.7 161194	2	AC021466	AC021466 Homo sapi
c 831	19	2.7 155824	2	AC087296	AC087296 Homo sapi	c 888	19	2.7 161218	2	AC119207	AC119207 Mus muscu
c 832	19	2.7 155889	2	BX120012	BX120012 Danio rer	c 889	19	2.7 161391	9	AC021878	AC021878 Homo sapi
c 833	19	2.7 155892	9	ALJ35809	ALJ35809 Human DNA	c 890	19	2.7 161523	9	AC012186	AC012186 Homo sapi
c 834	19	2.7 155923	9	AC091181	AC091181 Homo sapi	c 891	19	2.7 161533	2	BX004628	BX004628 Homo sapi
c 835	19	2.7 155937	2	AC016341	AC016341 Homo sapi	c 892	19	2.7 161694	2	AC137339	AC137339 Rattus no
c 836	19	2.7 156232	2	BX640408	BX640408 Danio rer	c 893	19	2.7 161900	9	AC096729	AC096729 Homo sapi
c 837	19	2.7 156237	9	AC091973	AC091973 Homo sapi	c 894	19	2.7 162180	9	AC124287	AC124287 Homo sapi
c 838	19	2.7 156467	2	AC083771	AC083771 Homo sapi	c 895	19	2.7 162209	9	CNS01R1H	CNS01R1H Homo chr
c 839	19	2.7 156534	10	AC127552	AC127552 Mus muscu	c 896	19	2.7 162361	2	AC023779	AC023779 Homo sapi
c 840	19	2.7 156576	2	AP001371	AP001371 Homo sapi	c 897	19	2.7 162551	2	AC096880	AC096880 Pan trogl
c 841	19	2.7 156660	2	AC141763	AC141763 Apis mell	c 898	19	2.7 162692	5	BX005067	BX005067 Zebrafish
c 842	19	2.7 156706	10	AC102069	AC102069 Mus muscu	c 899	19	2.7 162763	9	ALJ59262	ALJ59262 Human DNA
c 843	19	2.7 156820	9	AC074323	AC074323 Homo sapi	c 900	19	2.7 163049	9	BS000182	BS000182 Pan trogl
c 844	19	2.7 156831	2	AC147086	AC147086 Homo sapi	c 901	19	2.7 163067	2	AC022959	AC022959 Homo sapi
c 845	19	2.7 156857	2	AC025375	AC025375 Homo sapi	c 902	19	2.7 163088	2	AC116681	AC116681 Mus muscu
c 846	19	2.7 156923	2	AC021256	AC021256 Homo sapi	c 903	19	2.7 163132	9	AC025038	AC025038 Homo sapi
c 847	19	2.7 157069	2	AC015671	AC015671 Homo sapi	c 904	19	2.7 163179	9	AC022541	AC022541 Homo sapi
c 848	19	2.7 157242	2	AC083821	AC083821 Homo sapi	c 905	19	2.7 163231	9	ALJ62575	ALJ62575 Human DNA
c 849	19	2.7 157289	2	AC021447	AC021447 Homo sapi	c 906	19	2.7 163331	9	AC092802	AC092802 Homo sapi
c 850	19	2.7 157332	9	AC095033	AC095033 Homo sapi	c 907	19	2.7 163417	9	AC005043	AC005043 Homo sapi
c 851	19	2.7 157406	2	AC124953	AC124953 Medicago	c 908	19	2.7 163500	2	AL450316	AL450316 Homo sapi
c 852	19	2.7 157559	2	AC020344	AC020344 Drosophill	c 909	19	2.7 163567	9	AC095925	AC095925 Papio anu
c 853	19	2.7 157657	2	AC102826	AC102826 Mus muscu	c 910	19	2.7 163687	3	AC008200	AC008200 Drosophill
c 854	19	2.7 157854	2	BX640501	BX640501 Danio rer	c 911	19	2.7 163947	2	AC010964	AC010964 Homo sapi
c 855	19	2.7 157921	2	AC027726	AC027726 Homo sapi	c 912	19	2.7 164008	9	AL445483	AL445483 Human DNA
c 856	19	2.7 157923	10	AC102431	AC102431 Mus muscu	c 913	19	2.7 164138	9	ALJ62386	ALJ62386 Human DNA
c 857	19	2.7 157972	9	HSDB872K7	HSDB872K7 Human DNA	c 914	19	2.7 164232	2	AC067792	AC067792 Homo sapi
c 858	19	2.7 158014	2	AC092413	AC092413 Fells cat	c 915	19	2.7 164269	9	AC007497	AC007497 Homo sapi
c 859	19	2.7 158338	2	AC024720	AC024720 Homo sapi	c 916	19	2.7 164434	2	AC009841	AC009841 Drosophill
c 860	19	2.7 158346	2	AC101299	AC101299 Mus muscu	c 917	19	2.7 164529	2	AC079975	AC079975 Homo sapi
c 861	19	2.7 158347	2	AC120891	AC120891 Rattus no	c 918	19	2.7 164554	2	AC084811	AC084811 Homo sapi
c 862	19	2.7 158390	9	AC138942	AC138942 Homo sapi	c 919	19	2.7 164801	2	AC144793	AC144793 Mus muscu
c 863	19	2.7 158524	2	AC073839	AC073839 Homo sapi	c 920	19	2.7 164889	2	AC132534	AC132534 Rattus no
c 864	19	2.7 158702	9	AC104472	AC104472 Homo sapi	c 921	19	2.7 164933	2	AC074231	AC074231 Homo sapi
c 865	19	2.7 158735	2	AC104484	AC104484 Sus scrof	c 922	19	2.7 165047	9	AC079835	AC079835 Homo sapi
c 866	19	2.7 158749	2	AC091630	AC091630 Homo sapi	c 923	19	2.7 165193	9	AC010596	AC010596 Homo sapi
c 867	19	2.7 158787	9	AC010886	AC010886 Homo sapi	c 924	19	2.7 165415	9	ALJ359181	ALJ359181 Human DNA
c 868	19	2.7 159020	2	AC027023	AC027023 Homo sapi	c 925	19	2.7 165617	2	ALJ36381	ALJ36381 Homo sapi
c 869	19	2.7 159201	2	BX649485	BX649485 Danio rer	c 926	19	2.7 165727	9	AC099623	AC099623 Mus muscu
c 870	19	2.7 159365	10	ALJ94869	ALJ94869 Mouse DNA	c 927	19	2.7 165840	2	AC068112	AC068112 Homo sapi
c 871	19	2.7 159581	2	ALJ954356	ALJ954356 Homo sapi	c 928	19	2.7 165933	1	AP004174	AP004174 Mycoplasm
c 872	19	2.7 159698	5	ALB08019	ALB08019 Zebrafish	c 929	19	2.7 165990	2	AC142089	AC142089 Danio rer
c 873	19	2.7 159704	9	AC106000	AC106000 Homo sapi	c 930	19	2.7 166074	5	ALB45507	ALB45507 Zebrafish
c 874	19	2.7 159777	9	AC015883	AC015883 Homo sapi	c 931	19	2.7 166113	2	AC114256	AC114256 Rattus no
c 875	19	2.7 159919	9	ALJ359194	ALJ359194 Human DNA	c 932	19	2.7 166490	9	ALJ39438	ALJ39438 Human DNA
c 876	19	2.7 160370	9	AC023464	AC023464 Homo sapi	c 933	19	2.7 166366	8	AP005332	AP005332 Oryza sat
c 877	19	2.7 160378	2	AC090076	AC090076 Homo sapi	c 934	19	2.7 166576	5	BX005141	BX005141 Zebrafish
c 878	19	2.7 160450	2	AP005394	AP005394 Oryza sat	c 935	19	2.7 166694	3	AC008365	AC008365 Drosophill
c 879	19	2.7 160531	2	AC129090	AC129090 Medicago	c 936	19	2.7 166694	5	AC005050	AC005050 Zebrafish
c 880	19	2.7 160676	9	AC146170	AC146170 Pan trogl	c 937	19	2.7 166702	2	EX649633	EX649633 Danio rer
c 881	19	2.7 160746	2	AC044853	AC044853 Homo sapi	c 938	19	2.7 166762	2	AC035832	AC035832 Homo sapi
c 882	19	2.7 160780	2	AL444653	AL444653 Homo sapi	c 939	19	2.7 166843	9	AC090821	AC090821 Homo sapi
c 883	19	2.7 160814	2	AC119545	AC119545 Rattus no	c 940	19	2.7 166928	2	AC055861	AC055861 Homo sapi
c 884	19	2.7 160979	2	AC055879	AC055879 Zebrafish	c 941	19	2.7 166939	2	AC141016	AC141016 Rattus no
c 885	19	2.7 161142	5	BX004969	BX004969 Zebrafish	c 942	19	2.7 166963	10	ALJ29569	ALJ29569 Mouse DNA
c 886	19	2.7 161185	2	AC135798	AC135798 Medicago	c 943	19	2.7 166963	10	ALJ29569	ALJ29569 Mouse DNA

ALIGNMENTS					
RESULT 1					
BD245275					
LOCUS	714 bp	DNA	linear	PAT 17-JUL-2003	
DEFINITION	Development of novel antibiotics based on bacteriophage genomics.				
ACCESSION	BD245275				
VERSION	BD245275.1 GI:33055045				
KEYWORDS	JP 2002531107-A/10.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 714)				
AUTHORS	Pelletier,J., Gros,P. and Dubow,M.				
TITLE	Development of novel antibiotics based on bacteriophage genomics				
JOURNAL	Patent: JP 2002531107-A 10 24-SEP-2002; PHARTECH INC				
COMMENT	OS Staphylococcus aureus bacteriophage 77 PN JP 2002531107-A/10 PD 24-SEP-2002 PF 03-DEC-1999 JP 2000585456 PR 03-DEC-1998 US 60/110992;03-JUN-1999 US 09/326144 PR 28-SEP-1999 US 09/407804;30-SEP-1999 US 60/157218 PR 01-DEC-1999 US 60/168777;02-DEC-1999 US 09/454232 PI JERRY PELLETIER, PHILIPPE GROS, MICHAEL DUBOW PC C12N15/09,A01N63/00,A6K38/00,A6K45/00,A6P31/04,C07K14/005, PC C12M1/00, PC C12M1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC C12N15/00, PC A6I37/02 CC Coding Sequence FH Key Location/Qualifiers FT source 1..714 FT /organism='Staphylococcus aureus bacteriophage 77'. Location/Qualifiers 1..714 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"				
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source					
ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 9e-299;			
Matches 714;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 ATGAGCGCATATATGAAAAAAGCATTAATAATTTAAAAAATTCTGGAAATCAAAATTTT 60				
Db	1 ATGAGCGCATATATGAAAAAAGCATTAATAATTTAAAAAATTCTGGAAATCAAAATTTT 60				
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Db	61 AAAAAGTTAGATTCAGATATTCATCTATTCTCAAAGAATTGAAGGTGAAAAAACCAT 120				

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DB 121 AAGGTTTTCACAAAGTTTAAACAGAGAAAGTTTGTGAGATTGGTAAAC 180
QY 181 GTTAATTAAGAAATTTCTAATTCACACTTTCGATAGATGATTAATGATTTAT 240
DB 181 GTTAATTAAGAAATTTCTAATTCACACTTTCGATAGATGATTAATGATTTAT 240
QY 241 ACGAGATATAGTAATGTTATTCCTTATCCTTAAGAAACAAAAGATTAAAG 300
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RESULT 2
BD245281/c 41708 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281.1 GI:33055051
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 SEP-2002;
PNA-BIO-TECH INC

COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILLIPPE GROS, MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage /organism="Staphylococcus
77".
FEATURES
source Location/Qualifiers
1..41708
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 714; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 4e-238;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCGATATATAGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
DB 23982 ATGAGCGATATATAGAAACCAATTAATTAATTAATTAATTAATTAATTAAT 60
QY 61 AAAAAATTAGATTCAGATATTCATATTACTCAGAGATTGAAGTGAACCAAT 120
DB 23922 AAAAAATTAGATTCAGATATTCATATTACTCAGAGATTGAAGTGAACCAAT 120
QY 121 AAGGTTTTCACAAAGTTTAAACAGAGAAAGTTTGTGAGATTGGTAAAC 180
DB 23862 AAGGTTTTCACAAAGTTTAAACAGAGAAAGTTTGTGAGATTGGTAAAC 180
QY 181 GTTAATTAAGAAATTTCTAATTCACACTTTCGATAGATGATTAATGATTTAT 240
DB 23802 GTTAATTAAGAAATTTCTAATTCACACTTTCGATAGATGATTAATGATTTAT 240
QY 241 ACGAGATATAGTAATGTTATTCCTTATCCTTAAGAAACAAAAGATTAAAG 300
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DB 23682 ATGATTTTGAATTTGAAATGGAGATATTAATTAAGATGTTTTAAATTTAGCGCG 360
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DB 23622 CAAATTAATTCAGCTATATTAAGAAAGTTTGCATTAACAAAACAAACACA 420

QY 421 GATTCATCACTAAAGATTATTTATGATTTATATCTGATAGTTAGAAAT 480
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Db 23562 GAATTCATCACTAAAGATTATTTATGATTTATATCTGATAGTTAGAAAT 23503
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QY 481 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
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QY 661 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 714
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Db 23322 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23269
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RESULT 3
AR368770/c 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376552.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLES Compositions and methods involving an essential *Staphylococcus aureus* gene and its encoded protein
JOURNAL Patent: US 6376552-A 3 23-Apr-2002;
FEATURES
Location/Qualifiers
1. 41708
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 714; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 4e-298;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACGCAATAATAGAAAAAGCATTAAATTAATAAACTTCGAAATCCAAATTT 60
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Db 23982 ATGACGCAATAATAGAAAAAGCATTAAATTAATAAACTTCGAAATCCAAATTT 23923
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QY 61 AAAAGTTAGATTCAGATTCCTATTAATCTCAAGAGTTTGAAGGTGAAAAACAT 120
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Db 23922 AAAAGTTAGATTCAGATTCCTATTAATCTCAAGAGTTTGAAGGTGAAAAACAT 23863
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QY 121 AAAAGTTTATCCAAAGTTTAAACAGAGAAATAGTTTGTAGATTGGTATTAAC 180
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Db 23862 AAGGTTTTATCCAAAGTTTAAACAGAGAAATAGTTTGTAGATTGGTATTAAC 23803
QY 181 GTTAATTAAGAAATTTCTTAATTCACAGTTTCGAATAGATGAATAAAATGATTTCTAAT 240
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Db 23802 GTTAATTAAGAAATTTCTTAATTCACAGTTTCGAATAGATGAATAAAATGATTTCTAAT 23743
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QY 241 ACGAGATTAATAGTAATGTATTCCTTAATCCCTTAAGAAACAAAAGATTTAAAG 300
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Db 23742 ACGAGATTAATAGTAATGTATTCCTTAATCCCTTAAGAAACAAAAGATTTAAAG 23683
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QY 301 ATGAATTTGATTTGAATGGAGATTAATTAAGATGGTTTTTAATTAATTAAGCCGG 360
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Db 23682 ATGAATTTGATTTGAATGGAGATTAATTAAGATGGTTTTTAATTAATTAAGCCGG 23623
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QY 361 CAAATTAATTCAGCTATATTAAAGAGTTTGCATTAATAAATCCAAAAACACACAC 420
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Db 23622 CAAATTAATTCAGCTATATTAAAGAGTTTGCATTAATAAATCCAAAAACACACAC 23563
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QY 421 GAATTCATCACTAAAGATTATTTATGATTTATATCTGATAGTTAGAAAT 480
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Db 23562 GAATTCATCACTAAAGATTATTTATGATTTATATCTGATAGTTAGAAAT 23503
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QY 481 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
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Db 23502 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23443
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QY 541 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
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Db 23442 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23383
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QY 601 ATAGAAAGTTTACCAGAAATTAATTAATTAATTAATTAATTAATTAAT 660
|||||
Db 23382 ATAGAAAGTTTACCAGAAATTAATTAATTAATTAATTAATTAATTAAT 23323
|||||
QY 661 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 714
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Db 23322 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23269
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RESULT 4
DWC80H7 45861 bp DNA linear INV 27-Apr-1999
LOCUS DWC80H7
DEFINITION *Drosophila melanogaster* cosmid clone 80H7.
ACCESSION AL031027
VERSION AL031027.1 GI:3367670
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 45861)
AUTHORS Kottler, Cadelu, Dreano, Lelaure and Galibert, F.
TITLES Sequencing the distal X chromosome of *Drosophila melanogaster*
JOURNAL UPRI4 CNS Recombinations Genetiques, Universite de Rennes 1, 2 av
du Pr Leon Bernard, Faculte de Medecine, 35043 RENNES Cedex, France.

REFERENCE 2 (bases 1 to 45861)
AUTHORS Benos, P.
TITLE Direct Submission
JOURNAL Submitted (27-Apr-1999) European Drosophila Genome Sequencing Consortium
COMMENT On Aug 1, 1998 this sequence version replaced gi:3292887.
Sequence submitted by Takis Benos, EMBL Outstation - The EBI, Hinxton, Cambridge, CB10 1SD, U.K.
E-mail: benos@ebi.ac.uk on behalf of the European Drosophila Genome Sequencing Consortium. For further information see the European Drosophila Genome Sequencing Consortium's web site:
<http://edgp.ebi.ac.uk/>.

Coding sequences are predicted from computer analysis, using both gene and CDS prediction programs and matches to other sequences. These predictions and matches have been evaluated by the annotators and may have been refined by hand (in which case a GeneFinder prediction will have no score. The annotators have also used their judgement on what matches to represent in this record. A far more complete annotation record is available from FlyBase (<http://flybase.bio.indiana.edu/>) through the FlyBase Annotation Object linked by the db_xref qualifier in the Feature Table. The syntax for the representation of annotation used in this record is documented at:
<ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence/annotation/README>
IMPORTANT: This sequence is NOT necessarily the entire insert of clone 80H7. It may be shorter, since we are minimizing the overlap between clones to 100 bases, by trimming them. Clone 80H7 overlaps to the left with clone BAC032611 Clone 80H7 overlaps to the right with clone 196F3

The true right end of clone 80H7 is at position 101 of clone 196F3
Sequence in absolute orientation with respect to chromosome
Clone=80H7; Contig ID=1; Length=45861; Status=Finished.
Location/Qualifiers

FEATURES
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/db_xref="taxon:7227"
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target:EMBL:AI402932:137..309, score:'820.00'),
query:2231..2365, target:EMBL:AI402932:303..437,
score:'675.00'), (query:2428..2563,
target:EMBL:AI402932:435..570, score:'671.00'),
query:2622..2651, target:EMBL:AI402932:565..594,
score:'141.00'), method:'blastn', version:'1.4.9')"
/codon_start=1
/protein_id="CAB41536.1"

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score:'110.07')"
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method:'ppsearch')
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query:3349..3471, target:SMISS-PROT:P35038:174..134,
score:'176.00'), (query:3110..3184,
target:SMISS-PROT:P35038:235..211, score:'86.00'),
query:2990..3058, target:SMISS-PROT:P35038:272..230,
score:'71.00'), method:'blastx', version:'1.4.9')
species="MUS MUSCULUS (MOUSE)"
ranges:(query:3673..3771, target:SPTREMBL:008809:51..19,
score:'53.00'), (query:3349..3669,
target:SPTREMBL:008809:160..54, score:'147.00'),
query:3101..3184, target:SPTREMBL:008809:213..186,
score:'67.00'), (query:2972..3085,
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(query:5353..5802, target:EMBL:AA539009:235..684,
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SSLFLAVICFGCAVRMMVYKKNVAGSYALAVTFLMLGALALIQEARQA
YDAGEGRILVQKQKEKPEKQPRHHSSNSLDGY"
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GAMBIAE (AFRICAN MALARIA MOSQUITO)",
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score:"92.00"), (query:7545..7610,
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QLAGQITPPGKLCQVAGMGRTBOSSLNLTLANVSTIRHOTCMYIRSGLLPGMCA
GRLOGGTSCQSGGGRPLVHGRLVGVSWGCAEGLPGYVYDVEYRQMTIEGRSG
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complement(join(8190..8723,8888..9007,10469..10525))
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CDS
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 466 TTGCAATTGAAAATTAATTAAT 489
Db 34762 TTGCAATTGAAAATTAATTAAT 34785
RESULT 5
AC128735/c
LOCUS
DEFINITION
Drosophila melanogaster clone CH223-4018, *** SEQUENCING IN
PROGRESS ***, 4 unordered pieces.
AC128735
VERSION
AC128735.3 GI:22711522
KEYWORDS
HTG; HTGS PHASE1.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachyoptera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 62422)
REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshrocks,S.L., Amarutunge,H.C., Are,J.R., Ayala,M., Banks,T.,
Barbista,J., Benton,J., Bimago,K., Blankenburg,K., Bonnin,D.,
Bouck,O., Bowle,S., Britera,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dethorne,S.R., David,R.,
Devila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dihn,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Eamhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Geo,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlek,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Huliyil,S., Hume,J., Jackson,L.E.,
Jackson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., Kling,L., Korvah,J., Kover,C.,

Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtenberg, O., Liu, C., Liu, J., Liu, W., Loussaged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mashiney, E., McLeod, M.P., Meador, M., Mel, G., Metker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nkokenko, S., Ogih, M., Okunmu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Qullies, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shochat, N., Sisson, I., Sodergren, E., Sotake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umant, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Unpublished
2 (bases 1 to 62422)
Worley, K.C.
Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 62422)
Worley, K.C.
Direct Submission
Submitted (04-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2002 this sequence version replaced gi:22474839.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: DRP2
Center clone name: CH223-4018

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 60608 bases at least Q40
Consensus quality: 61160 bases at least Q30
Consensus quality: 61536 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2519: contig of 2519 bp in length
* 2520 2619: gap of unknown length
* 2620 6312: contig of 3693 bp in length
* 6313 6412: gap of unknown length
* 6413 21388: contig of 14976 bp in length
* 21389 21488: gap of unknown length
* 21489 62422: contig of 40934 bp in length.
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="CH223-4018"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 TTGAAATTGAAATTAATTAAT 489
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Db 47521 TTGAAATTGAAATTAATTAAT 47498

RESULT 6
AC017603
LOCUS
DEFINITION
AC017603
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC017603 74084 bp DNA linear HTG 10-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
AC017603
AC017603.1 GI:6554394
HTG: HTGS PHASE2.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Eurytomidae; Drosophilidae; Drosophila.
1 (bases 1 to 74084)
Adams, M. and Venter, J.C.
Direct Submission
Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA

COMMENT
This sequence was identified as CDM:10211430 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
1..74084
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/mol_type="genomic DNA"
/db_xref="taxon:7227"

ORIGIN

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 Best Local Similarity 100.0%; Pident.No. 5.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

466 TTGAAATTGAAATTTAAAT 489
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 Db 51791 TTGAAATTGAAATTTAAAT 51814

RESULT 7
 AC104141
 LOCUS
 DEFINITION Drosophila melanogaster X BAC RP86-9H15 (Roswell Park Cancer
 Institute Drosophila BAC Library) complete sequence.
 AC104141
 VERSION AC104141
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidae; Drosophilidae; Drosophila.

REFERENCE
 AUTHORS
 1 (bases 1 to 181360)
 Muzny,D., Scherer,S., Adams,M.D., Holt,R.A., Evans,C.A.,
 Gocayne,J.D., Tabor,P., Williamson,A., Homsi,F.H.,
 Dugan-Rocha,S.D., Sodergren,E.S., Hodgson,A.H., Chen,R.C.,
 Ayala,M., Scott,G.S., Worley,K.W., Amaratunga,P.G., Brandon,R.C.,
 Rogers,Y., An,H., Baldwin,D., Beeson,K.Y., Brown,M., Butney,C.,
 Busam,D.A., Cantor,A., Chen,G., Chen,Z., Clerc-Blanchard,K.,
 Davenport,L.B., Dietz,S.M., Ding,Y., Dodson,K., Doup,L.E.,
 Drepper,H., Emery-Cohen,A., Ferltera,S., Garg,N.D.S., Houck,J.,
 Hostin,D., Howland,T.J., Hume,J., Ibegwam,C., Jalali,M., Kovar,C.,
 Liu,W., Mantei,B., McIntosh,T.C., Morgan,M., Moy,M., Murphy,B.,
 Nelson,K.A., Ndassa,Y., Nguyen,N., Perez,L., Pittman,G.S., Puri,V.,
 Schaefer,F., Shen,H., Strong,R., Tector,C., Wang,Q., Williams,S.M.,
 Xiang,J., Zaveri,J.S., Zhou,J., Zorrilla,S., Smith,H.O.,
 Wheeler,D., Weinstein,G., Gibbs,R. and Venter,J.C.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Unpublished
 2 (bases 1 to 181360)
 Worley,K.C., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Albrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barbarta,J.,
 Benton,J., Bimaga,K., Blankenburg,K., Bonini,D., Bouck,J.,
 Bowie,S., Bileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
 Burch,P., Burgett,C., Burrell,K.L., Byrd,N.C., Carton,T.E.,
 Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
 Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
 Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
 Devy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
 Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Drepper,H.,
 Dugan-Rocha,S., Durbin,K.J., Earmhart,C., Edgar,D., Edwards,C.C.,
 Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
 Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
 Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
 Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,
 Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,

Hollins,B., Homsf., Howard,S., Huber,J., Huliy,S., Hume,J.,
 Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Joliver,S.,
 Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryak,J.,
 Kovar,C., Katoovic,J., Kuresh,A., Landry,N., Ieal,B., Lewis,L.C.,
 Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
 Louised,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
 Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
 Martinez,E., Massey,E., Mathiney,E., McLeod,M.P., Meador,M.,
 Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
 Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
 Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokoko,S.,
 Ogih,M., Okunou,G., Oreguene,N., Oviedo,R., Pace,A., Payton,B.,
 Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
 Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojudoan,I., Rolfe,M.,
 Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shooshari,N.,
 Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H.,
 Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
 Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
 Washington,S., Williams,G., Williamson,A., Wlezyk,R., Woodson,S.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Unpublished
 3 (bases 1 to 181360)
 Worley,K.C.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (05-DEC-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (11-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (01-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT
 On Jun 1, 2002 this sequence version replaced gi:18129379.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
 gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-36) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases.

Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu:8086/quality.info/genbank.annotation.htm.

FEATURES

source

Location/Qualifiers

1. 181360

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/db_xref="taxon:7227"

/chromosome="X"

/clone="RP98-9H15"

158548..158549

/note="Low quality, formally approved"

/function="low quality"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 TTACAAATTGAAAATAAATAAT 489

Db 172605 TTGAAATTGAAAATAAATAAT 172628

RESULT 8

AC15789/c

AC15789 206551 bp DNA linear HTG 17-FEB-2003

LOCUS Mus musculus clone RP23-398N2, WORKING DRAFT SEQUENCE, 15 ordered

DEFINITION pieces.

AC15789

VERSION
KEYWORDS
SOURCE
ORGANISM

AC15789.3 GI:28395901
HTG, HTGS PHASE2, HTGS DRAFT, HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

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JOURNAL

REFERENCE

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 206551)
Britten, B., Nussbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boudigault, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
Cook, A., Cooke, P., Dekarliano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faroo, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R.,
Lander, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Margis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meltrin, J., Menes, L.,
Mihova, T., Minge, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Traval, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 206551)
Britten, B., Nussbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T.,
Boudigault, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
Cook, A., Cooke, P., Dekarliano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faroo, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R.,
Lander, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Margis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meltrin, J., Menes, L.,
Mihova, T., Minge, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Traval, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (17-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 17, 2003 this sequence version replaced gi:21592066.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research.

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 123898

Center clone name: 398_N_2

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 203788 bases at least Q30

Consensus quality: 204444 bases at least Q20

Insert size: 205151; sum-of-contigs

Quality coverage: 10.6 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 15 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 2850: contig of 2850 bp in length
* 2851 2950: gap of 100 bp
* 2951 3647: contig of 697 bp in length
* 3648 3747: gap of 100 bp
* 3748 4411: contig of 664 bp in length
* 4412 4511: gap of 100 bp
* 4512 5700: contig of 1189 bp in length
* 5701 5800: gap of 100 bp
* 5801 7478: contig of 1678 bp in length
* 7479 7578: gap of 100 bp
* 7579 8461: contig of 883 bp in length
* 8462 8561: gap of 100 bp
* 8562 12189: contig of 3628 bp in length
* 12190 12289: gap of 100 bp
* 12290 18325: contig of 6036 bp in length
* 18326 18425: gap of 100 bp
* 18426 22438: contig of 4014 bp in length
* 22439 22539: gap of 100 bp
* 22540 27236: contig of 4697 bp in length
* 27237 43965: contig of 16629 bp in length
* 43966 44065: gap of 100 bp
* 44066 61489: contig of 17424 bp in length

FEATURES
source
* 61490 61589: gap of 100 bp
* 61590 78601: contig of 17012 bp in length
* 78602 78701: gap of 100 bp
* 78702 134900: contig of 56199 bp in length
* 134901 135000: gap of 100 bp
* 135001 206551: contig of 71551 bp in length.
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 330 TTGAAGTGTGTTTAAATTAA 353
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DB 10465 TTGAAGTGTGTTTAAATTAA 10442

RESULT 9	
AE003421	
LOCUS	304204 bp DNA linear INV 14-FEB-2003
DEFINITION	Drosophila melanogaster chromosome X section 5 of 74 of the complete sequence.
ACCESSION	AE003421 AE002566 AE014298
VERSION	AE003421.2 GI:22831488
KEYWORDS	
SOURCE	
ORGANISM	Drosophila melanogaster (fruit fly)
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrauloidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 304204)
AUTHORS	Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Aamundt,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Gall,J.R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blasei,R.G., Chapple,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,G., Abell,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballou,R.M., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolashikov,S., Borchen,D., Botchan,M.R., Bouck,J., Brocktein,P., Brotlier,P., Burke,K.C., Busan,D.A., Butler,H., Cadieu,E., Center,A., Chandrasekhar,I., Chertys,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davis,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evansgallita,C.C., Ferraz,C., Ferrieres,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Garg,N.S., Galtier,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Klenzmann,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Krat,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matal,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Mervilov,G., Mishina,N.V., Mohr,T.C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muszy,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusser,D.R., Paclob,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Poldr,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Sideras-Klimos,I., Slapton,M., Skupski,M.P., Smith,T., Spier,E., Spreading,A.C., Stepleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Westerman,D.A., Weinstock,G.M., Weisenbach,J., Williams,S.M., Woodgett,Morley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
TITLE	The genome sequence of Drosophila melanogaster
JOURNAL	Science 287 (5461), 2185-2195 (2000)
MEDLINE	20196006
PUBMED	10731132
REFERENCE	2 (bases 1 to 304204)

AUTHORS	Celniker,S.E., Adams,M.D., Kromtiller,B., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Aamundt,P.G., Brandon,R.C., Rogers,Y.H., Banzon,J., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busan,D.A., Carlson,J.W., Center,A., Chapple,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferrieres,S., Fritze,E., Gabor,G., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Matal,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Paclob,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stepleton,M., Strong,R., Svirskas,R., Tector,C., Tyler,D., Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.
TITLE	Sequencing of Drosophila melanogaster genome
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 304204)
AUTHORS	Mista,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L., Campbell,K., Hradecky,P., Huang,Y., Kamlirker,J.S., Prochnik,S.E., Smith,C.B., Tupy,J.L., Bergman,C.M., Benman,B.P., Carlson,J.W., Celniker,S.E., Clump,M.E., Dysgalad,R.A., Emerit,D., Fritze,E., de Grey,A.D.N.J., Harris,N.L., Kromtiller,B., Marshall,B., Millburn,G.H., Richter,J., Russo,S., Seearle,S.M.J., Smith,E., Shu,S., Smutnak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M., Rubin,G.M., Mungall,C.J. and Lewis,S.E.
TITLE	Annotation of Drosophila melanogaster genome
JOURNAL	Unpublished
REFERENCE	4 (bases 1 to 304204)
AUTHORS	Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
TITLE	Direct Submission
JOURNAL	Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
REFERENCE	5 (bases 1 to 304204)
AUTHORS	
CONSRTM	Direct Submission
JOURNAL	Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
REFERENCE	6 (bases 1 to 304204)
AUTHORS	
CONSRTM	Direct Submission
JOURNAL	Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
COMMENT	On Sep 13, 2002 this sequence version replaced gi:7290163.
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	/db_xref="FlyBase:FBgn0027793"

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NLEFQRLMRYERSDVQIVDARPLLENSADLERYVKEVEPSKNNILVNSDL
TEQQRHMALEYEUSEGIRTAFTSATLVEELKRAEECLDSFEPVQQLRAVEEIQS
LDSVEDALNVI EQYKTIPTQNDLPLRPDKNRSLSLLELLEFNITVGPRT
EQTAVGAGVYPNVGSSTINSILTVKVSATPCKTRQTLFLDKDILLCQPEL
VNESFVLTKADMLINGILPTIDQRHVPANVLCEPIPHVLEKNGYIVANPLEGD
MERPHSEELLAYGVNMGMTSNGQPOASARYVLAHYNGGLLYMSPSVQTE
YITPERQRRVYBESQLEGGQQRDAHINKSTSKELNQFSDKFTIAHVKGKTFPV
RLANDGSIVAGNDPAKWRHVRKEREKRLKKEFSLDEH"

gene
complement(3675..5752)
/gene="O-fut2"
/locus_tag="CG14789"
/note="last curated on Tue Jun 18 16:16:57 PDT 2002"
/map="2A4-2A4"

CDS
complement(127..987)
/gene="EG:BACN32G11.4"
/locus_tag="CG14787"
/product="CG14787-RA"
/db_xref="FLYBASE:FBgn0027793"
complement(183..965)
/gene="EG:BACN32G11.4"
/locus_tag="CG14787"
/note="EG:BACN32G11.4 gene product"
/codon_start=1
/product="CG14787-PA"
/protein_id="AAF45627.2"
/db_xref="GI:22831489"
/db_xref="FLYBASE:FBgn0027793"
/translation="MATESCKHRELVEEVSQGLHINFORMRRTLYELMALDL
ASADAVRVVLSGEFSAACGMEPLAKQGLNRSRTASHEAVSGDVEQYIH
EKXAFVRSIAKLIVHKLIVAFVRCVGLGLVCDLVFATVETLSAFVAFSH
LDCTKVGPMVPHVHMLRLGDASSIALCGIVASVREPEFMRVQYLRLP
SASLATKRLFRPQDLSLAELREGRPLAQRRLASSL"
complement(1300..3532)
/gene="EG:BACN32G11.5"
/locus_tag="CG14788"
/note="last curated on Tue Jun 18 16:17:21 PDT 2002"
/map="2A4-2A4"
/db_xref="FLYBASE:FBgn0027792"
complement(101n(1300..1632,1693..1898,1966..3259,
3334..3532))
/gene="EG:BACN32G11.5"
/locus_tag="CG14788"
/product="CG14788-RA"
/db_xref="FLYBASE:FBgn0027792"
complement(101n(1414..1632,1693..1898,1966..3259,
3334..3435))
/gene="EG:BACN32G11.5"
/locus_tag="CG14788"
/note="EG:BACN32G11.5 gene product"
/codon_start=1
/product="CG14788-PA"
/protein_id="AAF45628.1"
/db_xref="GI:7290165"
/db_xref="FLYBASE:FBgn0027792"
/translation="MGKNKGAPNIGRLKRFQHTQRKRVNDITMLTTELDGY
DWGRNLSTVESSFOFLRTAELAGTEFOAEKMTFPPVXORVGLSLKTEORAH
OKGDEHDOLKTPRRKWTETSAEIVRAENAFIDWRDLALGDEDEILTPYK
NLEFQRLMRYERSDVQIVDARPLLENSADLERYVKEVEPSKNNILVNSDL
TEQQRHMALEYEUSEGIRTAFTSATLVEELKRAEECLDSFEPVQQLRAVEEIQS
LDSVEDALNVI EQYKTIPTQNDLPLRPDKNRSLSLLELLEFNITVGPRT
EQTAVGAGVYPNVGSSTINSILTVKVSATPCKTRQTLFLDKDILLCQPEL
VNESFVLTKADMLINGILPTIDQRHVPANVLCEPIPHVLEKNGYIVANPLEGD
MERPHSEELLAYGVNMGMTSNGQPOASARYVLAHYNGGLLYMSPSVQTE
YITPERQRRVYBESQLEGGQQRDAHINKSTSKELNQFSDKFTIAHVKGKTFPV
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mRNA
/db_xref="FLYBASE:FBgn0027791"
complement(3675..5752)
/gene="O-fut2"
/locus_tag="CG14789"
/product="CG14789-RA"
/db_xref="FLYBASE:FBgn0027791"
complement(3827..5299)
/gene="O-fut2"
/locus_tag="CG14789"
/note="O-fut2 gene product"
/codon_start=1
/product="CG14789-PA"
/protein_id="AAF45629.1"
/db_xref="GI:7290166"
/db_xref="FLYBASE:FBgn0027791"
/translation="MRGSVRVLGMBGVYILYNVTSRGNLRDVTIRAVFYRLQ
TCVGFLOILPLPPTCPPEVLCMBGVYILYNVTSRGNLRDVTIRAVFYRLQ
RRRFRTYLVLPPIRPLVHMSQGLQSSLPWSHFDLASLRKAPVLDIEFLAQ
RLVNPQALVHVGNAFLQHYEVMLQGI FDKERTVLDKPCSGSLSGPILQAE
LIVGRFHCVRFGSAGLEKLEALIDEADPEVDMDRTYALSAETVLHDWDE
HFWQARSNRFAIRLEQVADPRQALDITDASAGVPPAWLELPRKNAKGSDYIC
AHLRRGDEVSRDATPTTLKAAQOVQOLRGENTVFLATATPYLELMEKLEYR
FRIYFAPESNVQRRELKQGVAVVDLNCVAVRYFVGYESTFTYRIYERELIEST
QASTFNTFCALGSCSRNAVPIVMADGSDSEEDSDPY"
6073..8012
/gene="EG:80H7.10"
/locus_tag="CG14777"
/note="last curated on Wed Jun 19 12:15:40 PDT 2002"
/map="2A4-2A4"
/db_xref="FLYBASE:FBgn0026872"
101n(6073..6293,7123..7284,7372..7505,7571..7702,
7767..8012)

gene
Query Match 3.4%; Score 24; DB 3; Length 304204;
Blast Local Similarity 100.0%; Pred. No. 3.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 466 TTGAAATTGAAATAATTAAT 489
DB 35189 TTGAAATTGAAATAATTAAT 35212

RESULT 10
HSA328489 729 bp DNA linear PRI 18-JUL-2002
LOCUS
DEFINITION
HSA328489
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 729)
Kutsenko,A.S., Gitzullin,R.Z., Al-Amin,A.N., Wang,F., Kvashta,S.M.,
Podowski,R.M., Matsushita,Y.G., Gyenchandani,A., Muravenko,O.V.,

Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashube, V.I., Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R. Not flanking sequences: a tool for gene discovery and verification of the human genome

JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)

MEDLINE 22131767

PUBMED 12136098

REFERENCE 2 (bases 1 to 729)

AUTHORS Zabarovsky, E.R.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2001) Microbiology and Tumoriobiology Centre, Karolinska Institute, Theorells väg, 3, Box 280, Stockholm 171 77, Sweden

FEATURES

source Location/Qualifiers

1..729

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="HSJ-6AC4RS"

ORIGIN

Query Match 3.2%; Score 23; DB 9; Length 729;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 TGATAGGTAAATAATTAAAG 550

|||||

DB 553 TGATAGGTAAATAATTAAAG 575

RESULT 11

AX346523 6254 bp DNA linear PAT 01-FEB-2002

LOCUS AX346523

DEFINITION Sequence 1594 from Patent WO0200928.

ACCESSION AX346523

VERSION AX346523.1 GI:18494409

KEYWORDS

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.

TITLE Diagnosis of diseases associated with the immune system

JOURNAL Patent: WO 0200928-A 1594 03-JAN-2002;

EpiGenomics AG (DE)

FEATURES

Location/Qualifiers

1..6254

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 3.2%; Score 23; DB 6; Length 6254;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 TATTAAAGTTGTTTAAATT 350

|||||

DB 957 TATTAAAGTTGTTTAAATT 979

RESULT 12

AF442957 14535 bp DNA circular INV 21-JAN-2002

LOCUS AF442957

DEFINITION Ostrinia nubilalis mitochondrial, complete genome.

ACCESSION AF442957

VERSION AF442957.1 GI:18252407

KEYWORDS

SOURCE mitochondrion Ostrinia nubilalis (European corn borer)

ORGANISM Ostrinia nubilalis

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea; Pyralidae; Pyraustinae; Ostrinia.

1 (bases 1 to 14535)

Coates, B.S. and Hellmich, R.L.

Near complete mitochondrial DNA sequence from Ostrinia nubilalis

Unpublished

2 (bases 1 to 14535)

Coates, B.S. and Hellmich, R.L.

Direct Submission

Submitted (04-NOV-2001) Entomology, Iowa State University, USDA-ARS, Corn Insects & Crop Genetics Research Unit, 111 Genetics Lab, Ames, IA 50011, USA

Genome sequence lacks part of non-coding region.

FEATURES

source Location/Qualifiers

1..14535

/organism="Ostrinia nubilalis"

/organeller="mitochondrion"

/mol_type="genomic DNA"

/db_xref="taxon:29057"

/country="USA: Ames, IA"

/notes="biotype: bivoltine 2"

<1..32

/product="tRNA-Met"

/note="codons recognized: AUR"

34..101

/product="tRNA-Ile"

/note="codons recognized: AUY"

complement(102..170)

/product="tRNA-Gln"

/note="codons recognized: CAR"

233..1234

/gene="ND2"

233..1234

/gene="ND2"

/codon_start=1

/transl_table=5

/product="NADH dehydrogenase subunit 2"

/protein_id="AAL66238.1"

/db_xref="gi:18252408"

/translation="MNSNKKFFFFIFLFFSTLSSNSNMGCGTGLEINLSTPIIN NSNNILSEASLAKFTFTQASININLFCITIKWMLAKRFENNTIIMNNSLLMG SAPHFEFPIIIEGLSWFNSFTLMTWKISPMILLSYWNNFLILIIILINSIIIGIG

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 1242..1308
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 /note="codons recognized: UGR"
 1302..1364
 /product="tRNA-Cys"
 /note="codons recognized: UGY"
 complement(1368..1430)
 /product="tRNA-Tyr"
 /note="codons recognized: UAY"
 <1442..2977
 /gene="COI"
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 /codon_start=1
 /transl_table=5
 /product="cytochrome c oxidase subunit 1"
 /protein_id="AAL66239.1"
 /db_xref="GI:18252409"
 /translation="RKMLSTNHKDI GTLVITFGISGAVGTSLILRAELQPSL
 IGDQIINTVTAAH IMIEFMVPMIGGFQWMLVPLGAPMAFPRMNNMSWIL
 PPSLTLISSIVENGAGTGVYPPSSINAHGSSVDLAIFSLHAGISSILGAIN
 FITTLINNRINGSPDQPLEFWSVGTALLLLSLPLVAGAFMLTTRNLTSPED
 PAGGDDPLVQHLFWFEGHEVYLILPFGMTSMLSQSGKKETFGSLGMYAMA
 IGLGFWMAHKEFTVGKIDTRAYTSATMIIVTGIKFSMLATLHQVINYSS
 IIMS LGRTLETYGGTGVLANPSIDIALHDYVVAHFVLSMGAVFALIGFTH
 WYPLETGLSNIPYFLKIQFTNFIQVNLTFPHQFTGLAGPRVSDVDAYISMTI
 SSLGSYISLLAGLILILIIWESMINQRMILFSINTLSWENYQILPPAHSYNELPIL
 SNF"
 2973..3039
 /product="tRNA-Leu"
 /note="codons recognized: UUR"
 3040..3721
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 3040..3721
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 /note="TAA stop codon is completed by the addition of 3' A
 residues to the mRNA"
 /codon_start=1
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 /transl_table=5
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 /protein_id="AAL66240.1"
 /db_xref="GI:18252410"
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 LFNNYINRFLAQMLELWITIPALITLIFALPSLRLLYLDELNRPLITLSIGH
 QWWSYSDNNIEFDSTYTPNENKNNRRLLEVNRILIPNNQIQIOWTATDVI
 HSWTIPSLGVKGDANRGLNQTNFINRPGIFGQSEICGANNSPPIVESISIKN
 FINMINNYS"
 3722..3792
 /product="tRNA-Lys"
 /note="codons recognized: AAR"
 3792..3858
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 /note="codons recognized: GAY"
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 3858..4019
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 3858..4019
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 /protein_id="AAL66241.1"
 /db_xref="GI:18252411"
 /translation="WQMPINMMLSLFEFFIVFIENINNYIFININNNYFENN
 KNNQIWKW"
 4013..4687
 /gene="ATP6"
 4013..4687
 /gene="ATP6"
 /codon_start=1
 /transl_table=5
 /product="ATP synthase subunit 6"
 /protein_id="AAL66242.1"
 /db_xref="GI:18252412"
 /translation="WMTNLESI FDSPTNLSLNWLSITIIGLMEIPYSFWLIPNRYF
 IENFIINNIHKEFRMLNGNSGTIFISNPTLENNFLGFYIFSTSLTMS
 LSIPLMSTFMEYGMINTQHMFIHMI PQGPTIIVPMVLIETISNI IPQGTIAVR
 LTAANIAGHLMTLLSGTNSLSYTMII LLVITQILLLIESNAVIGSYVIAISTL
 YSSRN"
 4687..5478
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 4687..5478
 /gene="COI11"
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 /transl_table=5
 /product="cytochrome c oxidase subunit 3"
 /protein_id="AAL66243.1"
 /db_xref="GI:18252413"
 /translation="KKNFYSHPYHIVDYSPPWITGALGVLLTGVWFHNNNL
 LMLGYIILITWYQWMDVSRGTFQKGTILVTKGLRWGMLIFISIFPSSPMA
 PFHSSLPNIEIGAMPNNIYVPRPQIPDLNTIILITISGVTVMHAIHANNQ
 MTQGLFETIIGITFTLQNYETLEAPFTIADSIIGSTFMAFGHGLHVMIGTWFL
 ICLRHINNQESNNHFGFEAAWYMHFVDVWVLELYISLYWGA"
 5481..5547
 /product="tRNA-Gly"
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 5551..5901
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 5551..5901
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 /codon_start=1
 /transl_table=5
 /product="NADH dehydrogenase subunit 3"
 /protein_id="AAL66244.1"
 /db_xref="GI:18252414"
 /translation="VLISYISIIIMMISNIMFSLIISKRSFSDRENKSPFECGDP
 KSSARIPISEFLITWIFLIPDEIALFPPMNLFKMTNFIIMTKISFFFIILIG
 LFEHNNQNLMTK"
 5912..5976
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 /note="codons recognized: GCN"
 tRNA
 3858..4019
 /gene="ATP8"
 3858..4019
 /gene="ATP8"
 /codon_start=1
 /transl_table=5
 /product="ATP synthase subunit 8"
 /protein_id="AAL66241.1"
 /db_xref="GI:18252411"
 /translation="WQMPINMMLSLFEFFIVFIENINNYIFININNNYFENN
 KNNQIWKW"
 4013..4687
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 4013..4687
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 /codon_start=1
 /transl_table=5
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 /protein_id="AAL66242.1"
 /db_xref="GI:18252412"
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 IENFIINNIHKEFRMLNGNSGTIFISNPTLENNFLGFYIFSTSLTMS
 LSIPLMSTFMEYGMINTQHMFIHMI PQGPTIIVPMVLIETISNI IPQGTIAVR
 LTAANIAGHLMTLLSGTNSLSYTMII LLVITQILLLIESNAVIGSYVIAISTL
 YSSRN"
 4687..5478
 /gene="COI11"
 4687..5478
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 /codon_start=1
 /transl_table=5
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 /protein_id="AAL66243.1"
 /db_xref="GI:18252413"
 /translation="KKNFYSHPYHIVDYSPPWITGALGVLLTGVWFHNNNL
 LMLGYIILITWYQWMDVSRGTFQKGTILVTKGLRWGMLIFISIFPSSPMA
 PFHSSLPNIEIGAMPNNIYVPRPQIPDLNTIILITISGVTVMHAIHANNQ
 MTQGLFETIIGITFTLQNYETLEAPFTIADSIIGSTFMAFGHGLHVMIGTWFL
 ICLRHINNQESNNHFGFEAAWYMHFVDVWVLELYISLYWGA"
 5481..5547
 /product="tRNA-Gly"
 /note="codons recognized: GGN"
 5551..5901
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 5551..5901
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 /codon_start=1
 /transl_table=5
 /product="NADH dehydrogenase subunit 3"
 /protein_id="AAL66244.1"
 /db_xref="GI:18252414"
 /translation="VLISYISIIIMMISNIMFSLIISKRSFSDRENKSPFECGDP
 KSSARIPISEFLITWIFLIPDEIALFPPMNLFKMTNFIIMTKISFFFIILIG
 LFEHNNQNLMTK"
 5912..5976
 /product="tRNA-Ala"
 /note="codons recognized: GCN"

tRNA 5976. 6041
/product="tRNA-Arg"
/note="codons recognized: CQR"
tRNA 6041. .6107
/product="tRNA-Asn"
/note="codons recognized: AAY"
tRNA 6109. 6176
/product="tRNA-Ser"
/note="codons recognized: AGN"
tRNA 6177. .6242
/product="tRNA-Glu"
/note="codons recognized: GAR"
tRNA complement(6243. 6309)
/product="tRNA-Phe"
/note="codons recognized: UUY"
gene complement(6294. .8030)
/gene="ND5"
complement(6294. .8030)
/gene="ND5"

CDS
/codon_start=1
/trna1_table=5
/product="NADH dehydrogenase subunit 5"
/protein_id="AA166245.1"
/db_xref="GI:18252415"
/translation="MGFISFFFLFPPSLNFMVYFTMNIIITLLEPISRNLSV
IKSILLNMSLFLFMFVSLISVVIYKSKYNSSEINLRITLLVLLVLSITLIS
PNTVSLGMDGLVSTCLVITIVIKISVNAQGLTALSNNRIGDLFLVIGMMWNG
SNVYLFYLSFNVDYSNEMSIIMIIAMTSAQIPFSSMLPAMAAPTPVSAVHS
TLVTAQIYLLIRNFLLIDMFIKILLISGLTFVAGISANVEFDKRTIALSTLSQ
LGMASILSMGPEDLAFPHLLTHAMEKALPMCAVGTIMPMMDIODIRMGISNFP
MTSLGAVSNNAALCGIPFLAGVSKDITLLEWLSLNLNFIILLYISGGLMFSFR
LTMVLTINDNLLSTVNLXEDDFIMKSMILLFNSVSGSFLMILIESYPMFLPE
NMGWVTVSILQVFNQGVSNMNTSVNKLMTQNSFLCLMFMFVSLVGLNFY
FLNEQPMALNIDMGSSEMSQGMFIMKRTSILENLSMKNYKIYLFSPVIMFPL
IILMIFLYLNSL"
complement(8046. .8112)

Query Match 3.2%; Score 23; DB 3; Length 14535;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 GAAATTAATTAATAAATGA 497
|||||
DB 6388 GAAATTAATTAATAAATGA 6410

RESULT 13
AF467260 14536 bp DNA circular INV 21-JAN-2002
LOCUS Ostrinia furnacalis mitochondrion, complete genome.
DEFINITION AF467260
ACCESSION AF467260.1 GI:18252681
VERSION
KEYWORDS
SOURCE
ORGANISM
mitochondrion Ostrinia furnacalis (Asian corn borer)
Ostrinia furnacalis
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

REFERENCE
Pyralidae; Pyraustinae; Ostrinia.
1 (bases 1 to 14536)
AUTHORS Coates,B.S., Hellmich,R.L. and Lewis,L.C.
TITLE Near complete mitochondrial genome of Ostrinia furnacalis
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 14536)
TITLE Coates,B.S., Hellmich,R.L. and Lewis,L.C.
REFERENCE Submitted (10-JAN-2002) Corn Insects and Crop Genetics Research
Unit, USDA-ARS, 111 Genetics Lab/Iowa State University, Ames, IA
50011, USA
COMMENT
Genome sequence lacks part of non-coding region.
FEATURES
source
Location/Qualifiers
1. 14536
/organism="Ostrinia furnacalis"
/organeller="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:93504"
/country="China: Hengshui, Hebei province"
<1. .32
/product="tRNA-Met"
34. .101
/product="tRNA-Ile"
/note="codons recognized: AUY"
complement(102. .170)
/product="tRNA-Gln"
/note="codons recognized: CAR"
233. .1234
/gene="ND2"
233. .1234
/gene="ND2"
/codon_start=1
/trna1_table=5
/product="NADH dehydrogenase subunit 2"
/protein_id="AA166392.1"
/db_xref="GI:18252682"

tRNA
/product="tRNA-Met"
34. .101
/product="tRNA-Ile"
/note="codons recognized: AUY"
complement(102. .170)
/product="tRNA-Gln"
/note="codons recognized: CAR"
233. .1234
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233. .1234
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/db_xref="GI:18252682"

CDS

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complement(1302. .1364)
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complement(1302. .1364)
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/note="codons recognized: UAY"
<1442. .2977
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<1442. .2977
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/codon_start=1
/trna1_table=5

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/note="codons recognized: UGR"
complement(1302. .1364)
/product="tRNA-Tyr"
/note="codons recognized: UAY"
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/codon_start=1
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/product="cytochrome c oxidase subunit 1"
/protein_id="AAL66397.1"
/db_xref="GI:18252683"
/translation="RKMLYSTNHKDIGLVEIFGWSGAVGTSLILIRALNGPSL
IGDDQIVNTIVTVAHAFIMIFPMVPMIGGQMWLVPLDGAPMVAFPMNNNSFML
PSLILISSIVENGAGTGMVTPPLSNIAHGSSVDLAFSLHAGISIIIGAN
FTITINNRINGSPDOMPLFWSVGTALLLLSLPVALGATMLLTRNLTSTFD
PAGGDDPLVQHLFWFGHEVITILIDFGQMTSTISQSGKKEIFGSLAKIYAWMA
IGLGEVVAHMFVQMDIDTRAVTSTMTIAVPTGKIFSWLATLHQIVSPS
ILMSLGEVFLFTVGGITGVLANSSIDIALHDYVVAHFYVLSMGVFAIIAGFIH
WYPLFTGLNLPYFLKIQFTFHEIGVNLTFPQHFGLAGMPRVSDYDAISMNI
SSIGSYISLLAVMLILIIIMESMINQRMFLSLNLTSSIEWQNLPPAHSYNELPIL
SNF"
gene
2973..3039
/product="tRNA-Leu"
/note="codons recognized: UUR"
/db_xref="GI:18252683"
/gene="COI1"
3040..3721
/gene="COI1"
3040..3721
/note="TAA stop codon is completed by the addition of 3' A
residues to the mRNA"
/codon_start=1
/transl_except=(pos:3721,aa:TERM)
/transl_table=5
/product="cytochrome c oxidase subunit 2"
/protein_id="AAL66394.1"
/db_xref="GI:18252684"
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LFENKYNIRFLGQMLIWTIIPALIFIALPSLRLVLDLDRPLTLKSGH
QWWSYEYSDNENFESDYTPNENKNNRNLLEVDNRITLPMNNQIOWATATDI
HSMTPLSGYVDNANPGRILNQTNFINRPGIFGQCEICGANSMPYVESISIN
FINMINYS"
tRNA
3722..3792
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/note="codons recognized: AAR"
3792..3861
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/protein_id="AAL66395.1"
/db_xref="GI:18252685"
/translation="VQWMPINMGLSLFFIILFIENINMYIIFINNNNNYFRNN
KNNQIWMW"
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4016..4690
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CDS

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/db_xref="GI:18252686"
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LSISLPNLSFEGYQMLANTQRMFIHPIRGPTTILRFNVLLETISNIIRGGLAVR
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MTQGLFTIILIGIYFTFLDAYEYLAFTIADSIYGSTFMAFGHGLPMI GTMEL
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/db_xref="GI:18252688"
/translation="MILISYISIIIMISNIMMFLSIIISKSFSDREKNSPEEGFD
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GLFENNMMLMTK"
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5982..6044
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/note="codons recognized: CGN"
6046..6112
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/note="codons recognized: AAY"
6114..6181
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/note="codons recognized: AGN"
6182..6247
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CDS

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 /db_xref="GI:18252689"
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 IMSILLDMSLFPMFVSILISVYIYKRSYMASEINLREIIVLLEFVSKILLIS
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 SNVYLFYLSFMNDISPEMISIMIIAMTKSAQIPFSSWLPAAAPVPSALVSS
 TLVTAGIYLLIRENILLIDMFSEKILLISGLTFPAAGISANVEFDLKRILASTVQ
 LGMGSIIISWMPDLAFPHLLTHAMEKALLPMCAGYIHPAQDIOIRMGGISNFI
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 NMGWVIVSILGVFMGFIISNNIYSNKRILWYQISNPLCLMFMPLSTYGLNFY
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 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 GAAATTAATTAATTAATGA 497
 DB 6393 GAAATTAATTAATTAATGA 6415

RESULT 14
 AC122478 135772 bp DNA linear ROD 13-NOV-2003
 LOCUS Mus musculus BAC clone RP24-337D11 from chromosome 6, complete
 DEFINITION sequence.
 AC122478
 VERSION AC122478.3 GI:27877424
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Goyes, E. and Cotton, M.
 TITLE The sequence of Mus musculus BAC clone RP24-337D11
 JOURNAL Unpublished (2001)
 REFERENCE 2 (bases 1 to 135772)
 AUTHORS Wilson, R.
 TITLE Sequencing of Mus musculus
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 135772)
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 135772)
 AUTHORS McPherson, J.D. and Waterston, R.H.

TITLE Direct Submission
 JOURNAL Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park
 REFERENCE Parkway, St. Louis, MO 63108, USA
 AUTHORS 5 (bases 1 to 135772)
 TITLE McPherson, J.D. and Waterston, R.H.
 JOURNAL Direct Submission
 REFERENCE Submitted (23-JUN-2003) Genome Sequencing Center, 4444 Forest Park
 AUTHORS Parkway, St. Louis, MO 63108, USA
 TITLE 6 (bases 1 to 135772)
 JOURNAL Wilson, R.
 REFERENCE Direct Submission
 AUTHORS Submitted (13-NOV-2003) Department of Genetics, Washington
 TITLE University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 JOURNAL On Jan 23, 2003 this sequence version replaced gi:21539177.
 COMMENT ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Gencenter code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submissions@wustl.wustl.edu
 Summary Statistics
 Center project name: M_BB0337D11

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Was Warren,
 Department of Genetics, Washington University, St. Louis MO. For
 additional information about the map position of this sequence, see
 http://genome.wustl.edu

SOURCE INFORMATION:
 The RPI-24 BAC library has been constructed by Pieter de Jong and
 coworkers (http://www.choil.org) from male C57BL/6J mouse spleen
 and/or brain genomic DNA. The clone and detailed information can be
 obtained from Pieter de Jong and coworkers at http://www.choil.org

NEIGHBORING SEQUENCE INFORMATION:
 This sequence is the entire insert of the clone.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
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4177. .4415		19673. .19782	/rpt_family="Alu"
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4430. .4344		19825. .19945	/rpt_family="Alu"
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4609. .4675		20386. .20521	/rpt_family="I1"
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11481. .11660			
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11661. .11730			
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14818. .14899			
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Query Match 3.2%; Score 23; DB 10; Length 135772;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 AACGTAAATAATTAAGGTAA 554
Db 98676 AACGTAAATAATTAAGGTAA 98698

RESULT 15
AC105750/c 166478 bp DNA linear PRI 24-MAY-2002
LOCUS AC105750 Homo sapiens chromosome 3 clone RP11-776K4, complete sequence.
ACCESSION AC105750
VERSION AC105750.2 GI:21166210
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Scaphimachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
Haugen,E.D.
1 (bases 1 to 166478)

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166478)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 166478)

REFERENCE
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Scaphimachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 24, 2002 this sequence version replaced gi:18093011.

----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchga@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP11-776K4 (bc0559)

----- Summary Statistics
Sequencing vector: plasmid; 92% of reads
Sequencing vector: plasmid; 108752; 8% of reads
Chemistry: Dye-terminator Big Dye; 35% of reads

Assembly program: Phrap; version 0.990319
Consensus quality: 166291 bases at least Q40
Consensus quality: 166469 bases at least Q30
Consensus quality: 166478 bases at least Q20
Insert size: 166478; sum-of-contigs
Quality coverage: 8.3k in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': Mapping in progress
3': RP11-45415 (UWGC:bc0430) AC105933

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI		HindIII		BglII	
SeqDerMap	FingerPrint	SeqDerMap	FingerPrint	SeqDerMap	FingerPrint
-----	-----	-----	-----	-----	-----
8696	8685	3818	3753	2920	2912
-----	-----	-----	-----	-----	-----
6	<800	6382	6487	2067	2109
-----	-----	-----	-----	-----	-----
739	<800	512	<800	9429	9669
-----	-----	-----	-----	-----	-----
5224	5154	449	<800	1306	1267
-----	-----	-----	-----	-----	-----
2145	2232	3728	3753	749	746
-----	-----	-----	-----	-----	-----
1840	1803	1154	1210	3914	4005

1780	1803	1737	1744	10546	10528	1566	1528	4732	4691	165	<800
3529	3501	2366	2330	2306	2309	3021	3073	54	<800	2148	2109
3496	3501	5486	5496	3696	3646	5900	5891	57	<800	123	<800
788	<800	1506	1543	4478	4365	178	<800	97	<800	4544	4365
4920	5154	749	763	8022	7999	1223	1207	3356	3478	2870	2912
581	<800	946	952	80	<800	1038	1036	1219	1210	1365	1351
526	<800	408	<800	913	915	3747	3720	247	<800	1060	990
284	<800	234	<800	6288	6265	2167	2232	2268	2330	2799	2737
1853	1803	3660	3753	1090	1080	448	<800	998	952	135	<800
496	<800	2283	2330	2565	2556	4511	4498	4814	4691	4143	4005
102	<800	1124	1101	6579	6492	4557	4498	3206	3321	3833	3817
313	<800	4364	4338	266	<800	5183	5154	2735	2735	21	<800
85	<800	1668	1647	4031	4005	2247	2232	752	<800	4769	4682
1361	1336	150	<800	2682	2737	926	942	2575	2735	5224	5128
1825	1803	3400	3478	2359	2309	7611	7547	3264	3321	3745	3646
12829	12923	2383	2330	2177	2109	101	<800	2766	2735	3877	3817
4548	4498	706	<800	975	990	1208	1207	1478	1429	983	990
1214	1207	787	<800	583	<800	1258	1207	1923	1874	11189	11246
2488	2553	293	<800	1796	1791	5815	5891	79	<800	6798	6823
774	<800	8394	8412	78	<800	392	<800	847	843	2675	2737
5997	5891	686	<800	1592	1574	2227	2232	2995	3082	4594	4365
3438	3501	581	<800	4358	4365	941	942	5728	5496		
3725	3720	1960	1966	1810	1791	4834	4823	5572	5496		
563	<800	3888	3753	7137	7042						
955	942	10610	10702	998	990						
1270	1207	621	<800	1941	1929						
181	<800	4019	3893	325	<800						
623	<800	202	<800	8061	7999						

Query Match 3.2% Score 23; DB 9; Length 166478;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 28 AATTAATTAATAACTCTGAAA 50
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 DB 35273 AATTAATTAATAACTCTGAAA 35251
 |||||

Search completed: October 15, 2004, 03:28:04
 Job time : 3746.62 secs

OM nucleotide - nucleotide search, using sw model

Run on: October 14, 2004, 18:55:29 ; Search time 476.318 Seconds

(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-B04A-4

Portect score: 714
Sequence: 1 atgacgcatactatagaaaa.....agatccctgataatagatga 714

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database :

- 1: N_Geneseq_29Jan04:*
- 2: geneseqn1980s:*
- 3: geneseqn1990s:*
- 4: geneseqn2000s:*
- 5: geneseqn2001as:*
- 6: geneseqn2002as:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	714	100.0	714	3	AA68248 Bacterioph
2	714	100.0	41708	3	AA68247 Bacterioph
3	714	100.0	41708	3	AA68247 Bacterioph
4	23	3.2	656	6	ABQ30760 Complete
5	23	3.2	656	6	ABQ30760 Complete
6	23	3.2	712	6	ABQ38659 Oligonuc
7	23	3.2	712	6	ABQ38658 Oligonuc

8	23	3.2	6254	6	AB133621 Human imm
9	22	3.1	6075	6	AB133550 Human imm
10	21	2.9	615	3	AAA43336 Xenopus s
11	21	2.9	2000	6	AB216393 Arabidops
12	21	2.9	5156	2	AA790505
13	21	2.9	5156	2	AA790505 Arabidops
14	21	2.9	5156	3	AA76122 Arabidops
15	21	2.9	6050	6	AB134011 Human imm
16	21	2.9	24389	4	AB129006 Drosophila
17	20	2.8	220	4	ABK42324 Genomic s
18	20	2.8	220	4	AAK85033 Human imm
19	20	2.8	220	4	AAK85031 Human imm
20	20	2.8	220	8	ABD60480 Connectiv
21	20	2.8	552	6	ABN89005 Human pro
22	20	2.8	583	6	ABQ47538 Oligonuc
23	20	2.8	583	6	ABQ47539 Oligonuc
24	20	2.8	695	3	AA713887 Aspergill
25	20	2.8	1271	2	AAK20327 Borrelia
26	20	2.8	1409	6	AB216176 Arabidops
27	20	2.8	2861	7	ACC48533 Stephyloc
28	20	2.8	3604	2	AAK13417 Enterococ
29	20	2.8	3604	6	ABN99212 Enterococ
30	20	2.8	4530	4	AB111726 Drosophila
31	20	2.8	5344	4	AB111976 Drosophila
32	20	2.8	6067	6	AB133185 Human imm
33	20	2.8	6067	6	AB192233 Chemical1
34	20	2.8	6067	6	AB192233 Chemical1
35	20	2.8	6134	6	AB133182 Human imm
36	20	2.8	7187	6	ABN80037 Human che
37	20	2.8	7203	6	AB134051 Human imm
38	20	2.8	7631	6	AB132860 Human imm
39	20	2.8	8883	4	AA546761 Human rep
40	20	2.8	11598	4	AA106652 Human rep
41	20	2.8	11598	5	AA540735 DNA encod
42	20	2.8	11600	4	AA106653 Human rep
43	20	2.8	11600	5	AA540736 DNA encod
44	20	2.8	12356	4	AA546509 Tumour su
45	20	2.8	14752	2	AAK20256 Borrelia
46	20	2.8	15109	2	AAV74355 Stephyloc
47	20	2.8	15121	6	ABN80239 Human che
48	20	2.8	30515	4	ABK42321 Genomic s
49	20	2.8	30515	4	AAK68732 Human imm
50	20	2.8	30515	4	AAK85029 Human imm
51	20	2.8	30515	8	ADB60477 Connectiv
52	20	2.8	110000	2	AAK20248_01
53	19	2.7	467	8	ACH33162 Human end
54	19	2.7	671	6	ABN64392 Human rib
55	19	2.7	807	6	ABN90764 Stephyloc
56	19	2.7	1220	6	AB157808 Murine AB
57	19	2.7	1869	4	AA105407 Human rep
58	19	2.7	2041	3	AA664194 Nucleotid
59	19	2.7	2291	6	AB157807 Murine AB
60	19	2.7	2682	2	AAV47539 Human ace
61	19	2.7	2682	2	AAV83610 Acetyl-co
62	19	2.7	2682	9	ADC01889 Human cIN
63	19	2.7	3424	5	ABV22643 Human pro
64	19	2.7	3424	5	ABV28466 Human pro

65	19	2.7	4040	4	AB111674	Ab111674 Drosophila	122	18	2.5	324	5	ABV49334	Abv49334 Human pro
66	19	2.7	4720	4	AB111074	Ab111074 Drosophila	123	18	2.5	339	4	AA125270	AA125270 Human bre
67	19	2.7	4720	4	AB116822	Ab116822 Drosophila	124	18	2.5	382	5	ABV56122	ABV56122 Human pro
68	19	2.7	4849	4	AB108580	Ab108580 Drosophila	125	18	2.5	385	7	ABR22768	ABR22768 Breast ca
69	19	2.7	5070	6	AB132800	Ab132800 Human lmm	126	18	2.5	400	5	ABV39012	ABV39012 Human pro
70	19	2.7	5266	6	AB132502	Ab132502 Human lmm	127	18	2.5	421	4	AA190919	AA190919 Human pro
71	19	2.7	5457	6	AB133131	Ab133131 Human lmm	128	18	2.5	425	4	AA189686	AA189686 Human pol
72	19	2.7	6089	4	AA546579	AA546579 Tumour su	129	18	2.5	429	5	ABV52842	ABV52842 Human pro
73	19	2.7	6089	4	AB133836	Ab133836 Human lmm	130	18	2.5	439	6	ABV61902	ABV61902 Human can
74	19	2.7	6195	6	AB132590	Ab132590 Human lmm	131	18	2.5	443	5	ABV05822	ABV05822 Human pro
75	19	2.7	6201	6	AB132496	Ab132496 Human lmm	132	18	2.5	446	7	AD557719	AD557719 BAC fragm
76	19	2.7	6453	6	AB067164	AB067164 Tumour su	133	18	2.5	456	7	AD441584	AD441584 Human sec
77	19	2.7	7069	4	AA566554	AA566554 Tumour su	134	18	2.5	459	6	ABV33688	ABV33688 Arabidops
78	19	2.7	7069	6	AB133353	Ab133353 Human lmm	135	18	2.5	464	5	ABV53314	ABV53314 Human pro
79	19	2.7	7069	6	AB131319	Ab131319 Signal tr	136	18	2.5	469	7	ABV74547	ABV74547 Human cDN
80	19	2.7	7069	6	AB170292	AB170292 Chemocali	137	18	2.5	477	7	ACA28748	ACA28748 Prokaryot
81	19	2.7	7069	6	AA561220	AA561220 Human gen	138	18	2.5	479	7	AD557720	AD557720 BAC fragm
82	19	2.7	7069	6	AB066984	AB066984 Human ang	139	18	2.5	479	7	AD441585	AD441585 Human sec
83	19	2.7	7321	6	ABK31424	AbK31424 Signal tr	140	18	2.5	484	8	ACH30458	ACH30458 Human tes
84	19	2.7	7321	6	AB170385	Ab170385 Chemocali	141	18	2.5	488	5	ABV02007	ABV02007 Human pro
85	19	2.7	7321	6	AA561337	AA561337 Human gen	142	18	2.5	491	5	ABV50972	ABV50972 Human pro
86	19	2.7	7922	6	ABN80086	ABn80086 Human che	143	18	2.5	502	4	AAK80308	AAK80308 Human lmm
87	19	2.7	8196	6	AB133092	Ab133092 Human lmm	144	18	2.5	511	6	ABQ48125	ABQ48125 Oligonuc1
88	19	2.7	8196	6	AB134538	Ab134538 Human met	145	18	2.5	524	4	AA120914	AA120914 Human bre
89	19	2.7	8196	6	AB170261	Ab170261 Chemocali	146	18	2.5	527	5	ABV23629	ABV23629 Human pro
90	19	2.7	8201	6	AB132306	Ab132306 Human lmm	147	18	2.5	527	5	ABV21263	ABV21263 Human pro
91	19	2.7	8201	6	AB154327	Ab154327 Chemocali	148	18	2.5	527	5	ABV23697	ABV23697 Human pro
92	19	2.7	8234	6	AB133649	Ab133649 Human lmm	149	18	2.5	527	5	ABV23697	ABV23697 Human pro
93	19	2.7	8905	2	AAK20263	AAK20263 Borella	150	18	2.5	528	6	ABQ45568	ABQ45568 Oligonuc1
94	19	2.7	9238	6	ABK28366	ABK28366 DNA trans	151	18	2.5	528	6	ABQ45568	ABQ45568 Oligonuc1
95	19	2.7	9254	9	AD854259	AD854259 Pretreate	152	18	2.5	530	5	ABV52716	ABV52716 Human pro
96	19	2.7	10241	4	AB110576	Ab110576 Drosophila	153	18	2.5	545	8	ACH40746	ACH40746 Human foe
97	19	2.7	11729	6	AB132895	Ab132895 Human lmm	154	18	2.5	561	8	ACH25146	ACH25146 Human adu
98	19	2.7	12007	6	AB132717	Ab132717 Human lmm	155	18	2.5	573	2	AAK61720	AAK61720 B. burgdo
99	19	2.7	12465	4	AA545326	AA545326 Chemocali	156	18	2.5	576	5	ABV38953	ABV38953 Human pro
100	19	2.7	12465	6	AB132634	Ab132634 Human lmm	157	18	2.5	576	5	ABV44740	ABV44740 Human pro
101	19	2.7	15674	6	AB132362	Ab132362 Human lmm	158	18	2.5	576	5	ABV39074	ABV39074 Human pro
102	19	2.7	15674	6	AB134476	Ab134476 Human met	159	18	2.5	576	5	ABV39074	ABV39074 Human pro
103	19	2.7	15674	6	AB170513	Ab170513 Chemocali	160	18	2.5	583	5	ABV32322	ABV32322 Human pro
104	19	2.7	15767	6	AB133207	Ab133207 Human lmm	161	18	2.5	587	4	AAK83844	AAK83844 Human lmm
105	19	2.7	15767	6	AB134553	Ab134553 Human met	162	18	2.5	606	2	AAK61719	AAK61719 B. burgdo
106	19	2.7	18218	6	AB133948	Ab133948 Human lmm	163	18	2.5	607	5	ABV51421	ABV51421 Human pro
107	19	2.7	18624	6	AB133702	Ab133702 Human lmm	164	18	2.5	609	5	ABV11991	ABV11991 Human pro
108	19	2.7	23024	4	AAE25499	AAE25499 Nucleotid	165	18	2.5	619	5	ABV11176	ABV11176 Human pro
109	19	2.7	24099	4	AA106944	AA106944 Human rep	166	18	2.5	623	3	AAK52778	AAK52778 Arabidops
110	19	2.7	92407	4	AAE28549	AAE28549 Genomic f	167	18	2.5	631	5	ABV41253	ABV41253 Human pro
111	19	2.7	110000	6	ABA03041_14	Continuation (15 o	168	18	2.5	631	5	ABV41253	ABV41253 Human pro
112	19	2.7	117574	6	AA145288	AA145288 Human KCN	169	18	2.5	631	5	ABV44798	ABV44798 Human pro
113	18	2.5	139	3	AA14458	AA14458 Human amy	170	18	2.5	631	5	ABV44860	ABV44860 Human pro
114	18	2.5	172	3	AAA41833	AAA41833 Human sec	171	18	2.5	658	7	AC094504	AC094504 Human col
115	18	2.5	201	4	AA112029	AA112029 Human bre	172	18	2.5	675	6	ABQ45851	ABQ45851 Oligonuc1
116	18	2.5	213	5	ABV19566	ABV19566 Human pro	173	18	2.5	691	5	ABV05697	ABV05697 Human pro
117	18	2.5	223	3	AAK24831	AAK24831 Human sec	174	18	2.5	694	6	ABQ42477	ABQ42477 Oligonuc1
118	18	2.5	240	5	ABV58851	ABV58851 Human pro	175	18	2.5	694	6	ABQ42476	ABQ42476 Oligonuc1
119	18	2.5	270	9	AD852380	AD852380 Primary r	176	18	2.5	722	5	ABV17698	ABV17698 Human pro
120	18	2.5	274	5	ABV58263	ABV58263 Human pro	177	18	2.5	742	4	AAK72035	AAK72035 Human lmm
121	18	2.5	277	5	ABV57365	ABV57365 Human pro	178	18	2.5				

c 179	18	2.5	752	6	ABQ27366	Abq27366	Oligonucle	c 236	18	2.5	3322	8	ABT43735	Abt43735	Molecule
c 180	18	2.5	752	6	ABQ27367	Abq27367	Oligonucle	c 237	18	2.5	3343	6	ABJ34136	Abj34136	Human imm
c 181	18	2.5	813	3	AA52520	Aa52520	Arabiidops	c 238	18	2.5	3353	1	AAH81234	Aah81234	Sequence
c 182	18	2.5	816	3	AA508436	Aa508436	Fusariolum	c 239	18	2.5	3353	2	AAO04496	Aao04496	Sequence
c 183	18	2.5	834	5	ABV14866	Abv14866	Human pro	c 240	18	2.5	3353	2	AAO14097	Aao14097	Amyloid p
c 184	18	2.5	884	4	ABV13933	Abv13933	Human bre	c 241	18	2.5	3353	2	AAO54258	Aao54258	Amyloid p
c 185	18	2.5	885	7	ACA34528	Ac34528	Prokaryot	c 242	18	2.5	3353	3	AAZ49951	Aaz49951	Human bet
c 186	18	2.5	931	5	ABV14926	Abv14926	Human pro	c 243	18	2.5	3354	2	AAZ32219	Aaz32219	Human bet
c 187	18	2.5	950	5	ABV60782	Abv60782	Human pro	c 244	18	2.5	3354	3	AAZ89477	Aaz89477	Human APP
c 188	18	2.5	1002	6	ABQ22125	Abq22125	Oligonucle	c 245	18	2.5	3354	7	ACC43142	Acc43142	Nucleotid
c 189	18	2.5	1002	6	ABQ22124	Abq22124	Oligonucle	c 246	18	2.5	3354	9	ADB33518	Adb33518	Human APP
c 190	18	2.5	1002	7	ACA27957	Ac27957	Prokaryot	c 247	18	2.5	3410	4	ABL24778	AbL24778	Human APP
c 191	18	2.5	1003	6	ABQ39670	Abq39670	Oligonucle	c 248	18	2.5	3435	7	ABK63219	Abk63219	Human cDN
c 192	18	2.5	1003	6	ABQ39671	Abq39671	Oligonucle	c 249	18	2.5	3447	4	ABJ09464	Abj09464	Drosophil
c 193	18	2.5	1168	2	AAI42750	Aai42750	Canarypox	c 250	18	2.5	3495	7	ACC68979	Acc68979	Human neu
c 194	18	2.5	1197	6	ABQ41306	Abq41306	Oligonucle	c 251	18	2.5	3520	2	AAW77504	Aaw77504	Human bet
c 195	18	2.5	1197	6	ABQ41307	Abq41307	Oligonucle	c 252	18	2.5	3521	2	AAI47554	Aai47554	H6 promot
c 196	18	2.5	1546	5	ABV21166	Abv21166	Human pro	c 253	18	2.5	3537	2	AAI69981	Aai69981	FLPV epik
c 197	18	2.5	1546	5	ABV26980	Abv26980	Human pro	c 254	18	2.5	3579	8	ABZ77538	Abz77538	Nucleotid
c 198	18	2.5	1586	6	ABV73415	Abv73415	Hexokinase	c 255	18	2.5	3585	5	AA583273	Aa583273	DNA encod
c 199	18	2.5	1614	2	AAQ67875	Aa67875	C6 Insect	c 256	18	2.5	3609	4	AAE28320	Aae28320	pJP107 do
c 200	18	2.5	1615	2	AAI04704	Aai04704	ALVAC C6	c 257	18	2.5	3621	5	ABV29298	Abv29298	Human pro
c 201	18	2.5	1615	2	AAI04704	Aai04704	ALVAC C6	c 258	18	2.5	3701	4	AAE55027	Aae55027	Nucleotid
c 202	18	2.5	1615	2	AAV26972	Aav26972	Canarypox	c 259	18	2.5	3701	4	AAE75820	Aae75820	ALVAC DNA
c 203	18	2.5	1615	2	AAZ08495	Aaz08495	Nucleotid	c 260	18	2.5	3701	4	AAE28310	Aae28310	Canarypox
c 204	18	2.5	1623	3	AAE22421	Aae22421	Human sec	c 261	18	2.5	3701	6	ABR15631	AbR15631	Canarypox
c 205	18	2.5	1680	9	AD556569	Ad556569	Rat gene	c 262	18	2.5	3706	2	AAI69995	Aai69995	Canarypox
c 206	18	2.5	1721	4	AAH45680	Aah45680	Human rib	c 263	18	2.5	3706	2	AAI47553	Aai47553	Canarypox
c 207	18	2.5	1801	3	AAAC36122	Aac36122	Arabiidops	c 264	18	2.5	3882	4	ABL05988	AbL05988	Drosophil
c 208	18	2.5	2000	6	ABE217169	Ab217169	Arabiidops	c 265	18	2.5	4174	4	ABL28076	AbL28076	Drosophil
c 209	18	2.5	2000	6	ABE215598	Ab215598	Arabiidops	c 266	18	2.5	4191	7	ACB31159	AbC31159	Prokaryot
c 210	18	2.5	2204	6	ABK15538	Abk15538	Canarypox	c 267	18	2.5	4434	2	AAV58240	Aav58240	ALVAC C6
c 211	18	2.5	2314	6	ABK34967	Abk34967	Human cDN	c 268	18	2.5	4434	2	AAV58245	Aav58245	K3L and E
c 212	18	2.5	2339	7	ACA45636	Ac45636	Canarypox	c 269	18	2.5	4434	2	AAV60253	Aav60253	K3L and E
c 213	18	2.5	2361	7	ACA48407	Ac48407	Prokaryot	c 270	18	2.5	4434	2	AAV60258	Aav60258	ALVAC C6
c 214	18	2.5	2369	6	ABK15634	Abk15634	Canarypox	c 271	18	2.5	4434	6	AAO67117	Aao67117	Human ang
c 215	18	2.5	2417	6	ABK15635	Abk15635	Canarypox	c 272	18	2.5	4434	6	AAI71985	Aai71985	Human ang
c 216	18	2.5	2430	4	AAH17380	Aah17380	Human cDN	c 273	18	2.5	4753	3	AAO67117	Aao67117	Human ang
c 217	18	2.5	2477	4	ABL08980	AbL08980	Drosophil	c 274	18	2.5	4909	2	AAI47558	Aai47558	Human ang
c 218	18	2.5	2486	3	AAV97037	Aav97037	Nucleotid	c 275	18	2.5	5181	6	ABL34103	AbL34103	Human imm
c 219	18	2.5	2520	4	AAE75827	Aae75827	Plasmid P	c 276	18	2.5	5348	4	ABL02884	AbL02884	Chemical
c 220	18	2.5	2520	4	AAE28317	Aae28317	pJP102 do	c 277	18	2.5	5397	6	ABL34204	AbL34204	Drosophil
c 221	18	2.5	2567	6	ABK15632	Abk15632	Canarypox	c 278	18	2.5	5447	4	AA546757	Aa546757	Human imm
c 222	18	2.5	2581	2	AAO13077	Aao13077	erica gene	c 279	18	2.5	5467	6	ABL34109	AbL34109	Tumour su
c 223	18	2.5	2615	6	ABK15633	Abk15633	Canarypox	c 280	18	2.5	5493	6	AA561386	Aa561386	Human imm
c 224	18	2.5	2731	2	AAZ77534	Aaz77534	Human ova	c 281	18	2.5	5525	6	ABK33930	AbK33930	Human gen
c 225	18	2.5	2769	4	AAE75830	Aae75830	Plasmid P	c 282	18	2.5	5525	6	ABL34463	AbL34463	Human DNA
c 226	18	2.5	3022	4	AA536553	Aa536553	Human car	c 283	18	2.5	5525	7	ADX20343	Adx20343	Prostate
c 227	18	2.5	3022	9	AD647247	Ad647247	Human car	c 284	18	2.5	5525	7	ADB84150	AdB84150	Human ren
c 228	18	2.5	3063	2	AAO67874	Aao67874	Canarypox	c 285	18	2.5	5530	6	ABK31443	AbK31443	Signal tr
c 229	18	2.5	3063	2	AAO68490	Aao68490	Nucleotid	c 286	18	2.5	5571	4	AA546483	Aa546483	Tumour su
c 230	18	2.5	3085	6	ABK15637	Abk15637	Canarypox	c 287	18	2.5	5571	6	ABK31346	AbK31346	Signal tr
c 231	18	2.5	3118	4	ABL24780	AbL24780	Drosophil	c 288	18	2.5	5571	6	ABJ70307	AbJ70307	Chemical
c 232	18	2.5	3129	3	AAZ62688	Aaz62688	Human sec	c 289	18	2.5	5571	6	AA561241	Aa561241	Human gen
c 233	18	2.5	3138	2	AAO11712	Aao11712	Shuttle v	c 290	18	2.5	5823	6	ABK28381	AbK28381	DNA trans
c 234	18	2.5	3238	5	AA583275	Aa583275	DNA encod	c 291	18	2.5	5883	6	ABL33732	AbL33732	Human imm
c 235	18	2.5	3302	4	ABL19744	AbL19744	Drosophil	c 292	18	2.5	5898	4	AA545471	Aa545471	Chemical

c 293	18	2.5	5898	6	ABL33940	Ab133940 Human Imm	c 350	18	2.5	6777	9	ADB47449	Abd47449 Human cDN
c 294	18	2.5	5898	6	ABK28329	Abk28329 DNA trans	c 351	18	2.5	6852	6	ABL70311	Ab170311 ChemCell
c 295	18	2.5	5938	6	ABN80218	Abn80218 Human che	c 352	18	2.5	6852	6	AA561249	AA561249 Human gen
c 296	18	2.5	5971	6	ABL32383	Ab132383 Human Imm	c 353	18	2.5	6917	6	ABL34234	Ab134234 Human Imm
c 297	18	2.5	6032	7	ABK77169	Abk77169 DNA sequ	c 354	18	2.5	6923	6	ABK31296	Abk31296 Signal tr
c 298	18	2.5	6042	6	ABO67042	Abog67042 Human ang	c 355	18	2.5	6923	6	ABL70275	Ab170275 ChemCell
c 299	18	2.5	6074	6	ABK33990	Abk33990 Human DNA	c 356	18	2.5	6923	6	AA561198	AA561198 Human gen
c 300	18	2.5	6074	7	ADK20378	Adk20378 Prostate	c 357	18	2.5	6934	6	ABL33390	Ab133390 Human Imm
c 301	18	2.5	6074	7	ADK64185	Adk64185 Human ren	c 358	18	2.5	7004	4	AA545412	AA545412 ChemCell
c 302	18	2.5	6079	6	ABL32258	Ab132258 Human Imm	c 359	18	2.5	7004	6	ABK28265	Abk28265 DNA trans
c 303	18	2.5	6090	2	AAT69977	Aat69977 FIVP modl	c 360	18	2.5	7312	6	ABL33814	Ab133814 Human Imm
c 304	18	2.5	6109	6	ABN80149	Abn80149 Human che	c 361	18	2.5	7312	6	ABL70401	Ab170401 ChemCell
c 305	18	2.5	6123	6	ABL33037	Ab133037 Human Imm	c 362	18	2.5	7312	6	AA561349	AA561349 Human gen
c 306	18	2.5	6144	2	AAT69976	Aat69976 FIVP splx	c 363	18	2.5	7352	6	ABL32370	Ab132370 Human Imm
c 307	18	2.5	6154	6	ABL33304	Ab133304 Human Imm	c 364	18	2.5	7508	6	ABK31207	Abk31207 Signal tr
c 308	18	2.5	6154	6	ABL33305	Ab133305 Human Imm	c 365	18	2.5	7508	6	ABL34130	Ab134130 Human Imm
c 309	18	2.5	6182	6	ABL34015	Ab134015 Human Imm	c 366	18	2.5	7644	6	ABL32530	Ab132530 Human Imm
c 310	18	2.5	6191	6	ABL33216	Ab133216 Human Imm	c 367	18	2.5	7990	6	ABL32159	Ab132159 Human Imm
c 311	18	2.5	6191	6	ABK31306	Abk31306 Signal tr	c 368	18	2.5	7990	6	ABL54308	Ab154308 ChemCell
c 312	18	2.5	6191	6	ABL70281	Ab170281 ChemCell	c 369	18	2.5	8044	4	AA546626	AA546626 Human gen
c 313	18	2.5	6191	6	ABN80160	Abn80160 Human che	c 370	18	2.5	8044	4	AA546657	AA546657 Human gen
c 314	18	2.5	6195	6	ABL32591	Ab132591 Human Imm	c 371	18	2.5	8420	4	ABK31324	Abk31324 Signal tr
c 315	18	2.5	6239	6	ABL33776	Ab133776 Human Imm	c 372	18	2.5	8420	6	ABL33976	Ab133976 Human Imm
c 316	18	2.5	6239	6	ABK28297	Abk28297 DNA trans	c 373	18	2.5	8456	3	AAA14873	AA14873 Nucleotid
c 317	18	2.5	6274	4	AA546321	AA546321 Tumour su	c 374	18	2.5	8648	6	ABL43177	Ab143177 Acabidiops
c 318	18	2.5	6274	6	ABK31238	Abk31238 Signal tr	c 375	18	2.5	8648	7	ABQ77909	Abq77909 Arabidops
c 319	18	2.5	6274	7	ADK20354	Adk20354 Prostate	c 376	18	2.5	8666	4	AA546305	AA546305 Human Imm
c 320	18	2.5	6274	7	ADK64161	Adk64161 Human ren	c 377	18	2.5	8666	6	ABL32396	Ab132396 Human Imm
c 321	18	2.5	6274	9	ADB54121	Adb54121 Pretreate	c 378	18	2.5	8666	6	ABK34008	Abk34008 Human DNA
c 322	18	2.5	6274	9	ADB54249	Adb54249 Pretreate	c 379	18	2.5	8666	6	ABQ67177	Abq67177 Human ang
c 323	18	2.5	6312	4	AA528998	AA528998 Genomic s	c 380	18	2.5	8666	9	ADB54111	ADB54111 Pretreate
c 324	18	2.5	6312	4	AA530241	AA530241 DNA encod	c 381	18	2.5	8666	9	ADB54239	ADB54239 Pretreate
c 325	18	2.5	6312	4	AA535075	AA535075 DNA #25 e	c 382	18	2.5	8666	9	ADE84177	AdE84177 Human Lym
c 326	18	2.5	6312	4	ABK06808	Abk06808 Human gen	c 383	18	2.5	8666	9	ADE84101	AdE84101 Human Lym
c 327	18	2.5	6312	4	AA162822	AA162822 Human gen	c 384	18	2.5	8758	6	ABL33118	Ab133118 Human Imm
c 328	18	2.5	6312	4	ABK44027	Abk44027 Genomic D	c 385	18	2.5	8867	9	ADE56784	AdE56784 Rat gene
c 329	18	2.5	6312	5	AA529742	AA529742 Human end	c 386	18	2.5	9007	4	AA546616	AA546616 Human ang
c 330	18	2.5	6312	6	ABT07833	Abt07833 Novel hum	c 387	18	2.5	9095	6	ABQ67061	Abq67061 Human ang
c 331	18	2.5	6312	6	ABV84145	Abv84145 Human pol	c 388	18	2.5	9577	9	ADC87604	Adc87604 Human GPC
c 332	18	2.5	6312	7	ACD01496	Acc01496 Human gen	c 389	18	2.5	9646	6	ABL33688	Ab133688 Human Imm
c 333	18	2.5	6312	9	ADC46517	Adc46517 Human neo	c 390	18	2.5	9725	6	ABL33292	Ab133292 Human Imm
c 334	18	2.5	6325	7	AB210086	Ab210086 Haematopo	c 391	18	2.5	9725	6	ABN80180	Abn80180 Human che
c 335	18	2.5	6325	7	AB210232	Ab210232 Haematopo	c 392	18	2.5	9830	4	AAK82379	AAK82379 Human Imm
c 336	18	2.5	6326	6	ABL210286	Ab192286 ChemCell	c 393	18	2.5	9964	6	ABL32098	Ab132098 Human Imm
c 337	18	2.5	6326	6	AB149357	Ab149357 Human pol	c 394	18	2.5	11029	4	AA546414	AA546414 Human gen
c 338	18	2.5	6326	6	ABD22337	Abd22337 ChemCell	c 395	18	2.5	11555	6	ABL32616	Ab132616 Human Imm
c 339	18	2.5	6397	6	ABL32819	Ab132819 Human Imm	c 396	18	2.5	11555	6	AAD28380	AA28380 Human che
c 340	18	2.5	6419	6	ABL32267	Ab132267 Human Imm	c 397	18	2.5	11662	6	ABL33900	Ab133900 Human Imm
c 341	18	2.5	6476	6	ABL32541	Ab132541 Human Imm	c 398	18	2.5	11812	4	AA545501	AA545501 ChemCell
c 342	18	2.5	6531	6	ABL32640	Ab132640 Human Imm	c 399	18	2.5	11812	4	AA546741	AA546741 Human gen
c 343	18	2.5	6577	6	ABL33357	Ab133357 Human Imm	c 400	18	2.5	11812	6	ABL34118	Ab134118 Human Imm
c 344	18	2.5	6577	6	ABL70362	Ab170362 ChemCell	c 401	18	2.5	11812	6	ABK28431	Abk28431 DNA trans
c 345	18	2.5	6577	6	AA561222	AA561222 Human gen	c 402	18	2.5	11976	6	ABL32594	Ab132594 Human Imm
c 346	18	2.5	6641	6	ABN80002	Abn80002 Human che	c 403	18	2.5	12409	6	AA563312	AA563312 ChemCell
c 347	18	2.5	6749	2	AAT47561	Aat47561 Cytochrome	c 404	18	2.5	12465	6	AA545327	AA545327 Human Imm
c 348	18	2.5	6749	2	AAT47564	Aat47564 Cytochrome	c 405	18	2.5	12465	6	ABL32635	Ab132635 Human Imm
c 349	18	2.5	6777	9	ADB47449	Adb47449 Human cDN	c 406	18	2.5	12574	4	AA105318	AA105318 Human rep

c 407	18	2.5	12574	4	ABL198187	Ab1198187 Human tes	c 464	18	2.5	56516	2	AAZ00870	Aaz00870 Fc1 genom
c 408	18	2.5	12501	6	ABL14207	Ab114207 Human imm	c 465	18	2.5	56520	2	AAZ01022	Aaz01022 Wild type
c 409	18	2.5	12733	6	ABL12091	Ab112091 Human imm	c 466	18	2.5	69327	6	AB555821	Ab555821 Human tra
c 410	18	2.5	12814	2	AAZ4730	Aaz4730 Swed1-sh-F	c 467	18	2.5	96389	8	ADB52675	Ad52675 Mouse Ttp
c 411	18	2.5	13069	4	AA536350	AA536350 Human car	c 468	18	2.5	96389	9	ADB72413	Ad72413 Mouse Top
c 412	18	2.5	13069	4	AAK74980	AAK74980 Human imm	c 469	18	2.5	96591	9	ADB85301	Ad85301 Mouse Sos
c 413	18	2.5	13069	9	AD647044	Ad647044 Human car	c 470	18	2.5	96592	8	ADB02822	Ad02822 Human SOS
c 414	18	2.5	13326	6	ABL131712	Ab1131712 Human imm	c 471	18	2.5	96592	9	ADB72560	Ad72560 Human SOS
c 415	18	2.5	13584	6	ABL12615	Ab112615 Human imm	c 472	18	2.5	96594	8	ADB72494	Ad72494 Human MOR
c 416	18	2.5	14253	6	ABL13494	Ab113494 Human imm	c 473	18	2.5	96594	9	ADB85236	Ad85236 Human MOR
c 417	18	2.5	14919	4	AA163992	AA163992 Human pol	c 474	18	2.5	96594	9	ADB85236	Ad85236 Human MOR
c 418	18	2.5	15121	6	ABN80238	Abn80238 Human che	c 475	18	2.5	110000	2	AAZ02063	Aaz02063 17
c 419	18	2.5	15121	6	ABN80238	Abn80238 Human che	c 476	18	2.5	110000	2	AAZ02063	Aaz02063 17
c 420	18	2.5	15587	6	ABK13143	Abk13143 Signal tr	c 477	18	2.5	110000	6	AB90521_15	Ab90521_15
c 421	18	2.5	15587	6	ABK13143	Abk13143 Signal tr	c 478	18	2.5	110000	6	AB90521_16	Ab90521_16
c 422	18	2.5	15587	6	ABK13143	Abk13143 Signal tr	c 479	18	2.5	110000	6	AB90521_14	Ab90521_14
c 423	18	2.5	15587	6	ABK13143	Abk13143 Signal tr	c 480	18	2.5	110000	6	AB90521_14	Ab90521_14
c 424	18	2.5	15692	2	AAZ4731	Aaz4731 London-FA	c 481	18	2.5	110000	7	ACF67195_2	Acf67195_2
c 425	18	2.5	15701	2	AAZ4732	Aaz4732 Swed1-sh-F	c 482	18	2.5	110000	7	ACF67383_1	Acf67383_1
c 426	18	2.5	15701	2	AAZ4733	Aaz4733 Swed1-sh-F	c 483	18	2.5	110000	7	ACF67383_2	Acf67383_2
c 427	18	2.5	15767	6	ABL133206	Ab1133206 Human imm	c 484	18	2.5	110000	7	ACF67387_4	Acf67387_4
c 428	18	2.5	16225	4	AAK73303	AAK73303 Human met	c 485	18	2.5	110000	7	ACF67387_4	Acf67387_4
c 429	18	2.5	16766	6	ABL14156	Ab114156 Human imm	c 486	18	2.5	113033	7	AAZ54213	Aaz54213
c 430	18	2.5	16994	6	ABL132989	Ab1132989 Human imm	c 487	18	2.5	125653	7	ABK71167	Abk71167
c 431	18	2.5	17131	6	ABL13052	Ab113052 Human imm	c 488	18	2.5	143899	6	AAZ138336	Aaz138336
c 432	18	2.5	17294	6	ABL132987	Ab1132987 Human imm	c 489	18	2.5	215980	6	AAZ138337	Aaz138337
c 433	18	2.5	17341	3	AAK14872	AAK14872 Genomic D	c 490	18	2.5	267156	6	ABL68560	Ab168560 Kidney ca
c 434	18	2.5	17341	3	AAK14872	AAK14872 Genomic D	c 491	18	2.5	349999	6	ADC87010	Adc87010 Human GPC
c 435	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 492	17	2.4	49	6	AACT6470	Aact6470
c 436	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 493	17	2.4	180	6	ABQ95184	Abq95184
c 437	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 494	17	2.4	180	6	ABQ95184	Abq95184
c 438	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 495	17	2.4	180	6	ABQ95184	Abq95184
c 439	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 496	17	2.4	180	6	ABQ95184	Abq95184
c 440	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 497	17	2.4	180	6	ABQ95184	Abq95184
c 441	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 498	17	2.4	180	6	ABQ95184	Abq95184
c 442	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 499	17	2.4	180	6	ABQ95184	Abq95184
c 443	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 500	17	2.4	180	6	ABQ95184	Abq95184
c 444	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 501	17	2.4	180	6	ABQ95184	Abq95184
c 445	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 502	17	2.4	180	6	ABQ95184	Abq95184
c 446	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 503	17	2.4	180	6	ABQ95184	Abq95184
c 447	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 504	17	2.4	180	6	ABQ95184	Abq95184
c 448	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 505	17	2.4	180	6	ABQ95184	Abq95184
c 449	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 506	17	2.4	180	6	ABQ95184	Abq95184
c 450	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 507	17	2.4	180	6	ABQ95184	Abq95184
c 451	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 508	17	2.4	180	6	ABQ95184	Abq95184
c 452	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 509	17	2.4	180	6	ABQ95184	Abq95184
c 453	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 510	17	2.4	180	6	ABQ95184	Abq95184
c 454	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 511	17	2.4	180	6	ABQ95184	Abq95184
c 455	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 512	17	2.4	180	6	ABQ95184	Abq95184
c 456	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 513	17	2.4	180	6	ABQ95184	Abq95184
c 457	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 514	17	2.4	180	6	ABQ95184	Abq95184
c 458	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 515	17	2.4	180	6	ABQ95184	Abq95184
c 459	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 516	17	2.4	180	6	ABQ95184	Abq95184
c 460	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 517	17	2.4	180	6	ABQ95184	Abq95184
c 461	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 518	17	2.4	180	6	ABQ95184	Abq95184
c 462	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 519	17	2.4	180	6	ABQ95184	Abq95184
c 463	18	2.5	17580	6	ABN80013	Abn80013 Human che	c 520	17	2.4	180	6	ABQ95184	Abq95184

c 521	17	2.4	366	4	AA114547	AA114547 Human bre	c 578	17	2.4	540	4	AB196471	AB196471 Human tes
522	17	2.4	379	2	AA103501	AA103501 Neisseria	c 579	17	2.4	543	4	AAK53569	AAK53569 Human tes
523	17	2.4	382	2	AA193549	AA193549 Human pol	c 580	17	2.4	550	6	ABQ40570	ABQ40570 Oligonuc
524	17	2.4	382	8	ACH49811	ACH49811 Human 1eu	c 581	17	2.4	550	6	ABQ40571	ABQ40571 Oligonuc
525	17	2.4	386	9	ADD71843	ADD71843 Human uri	c 582	17	2.4	551	6	ABQ45968	ABQ45968 Oligonuc
c 526	17	2.4	391	8	ACH47886	ACH47886 Human 1un	c 583	17	2.4	551	6	ABQ45969	ABQ45969 Oligonuc
527	17	2.4	396	6	AB232150	AB232150 Candida a	c 584	17	2.4	553	6	AA521852	AA521852 Human tes
c 528	17	2.4	397	7	ABK49507	ABK49507 Bovine ES	c 585	17	2.4	553	7	ACF72636	ACF72636 Stephyloc
529	17	2.4	401	4	AAK96626	AAK96626 Human neu	c 586	17	2.4	558	5	ABV47989	ABV47989 Human pro
530	17	2.4	401	4	AAK98119	AAK98119 Human neu	c 587	17	2.4	572	4	AAH01663	AAH01663 Microspor
531	17	2.4	401	6	ABT01396	ABT01396 Human neu	c 588	17	2.4	577	5	ABV24528	ABV24528 Human pro
532	17	2.4	401	6	ABT02889	ABT02889 Human neu	c 589	17	2.4	578	6	AAH63027	AAH63027 Human can
533	17	2.4	402	4	AA539276	AA539276 Novel hum	c 590	17	2.4	582	5	ABV49010	ABV49010 Human pro
534	17	2.4	414	4	AA117337	AA117337 Human bre	c 591	17	2.4	584	5	ABV53869	ABV53869 Human pro
535	17	2.4	418	4	AA182992	AA182992 Human pol	c 592	17	2.4	588	3	AAK98031	AAK98031 Human col
536	17	2.4	418	4	AA185620	AA185620 Human pol	c 593	17	2.4	588	4	AAH34440	AAH34440 Human col
c 537	17	2.4	423	3	AAA90522	AAA90522 Murine am	c 594	17	2.4	597	2	AAK88556	AAK88556 Human chr
538	17	2.4	428	4	AA109448	AA109448 Human bre	c 595	17	2.4	604	5	ABV53636	ABV53636 Human pro
c 539	17	2.4	433	2	AAQ59567	AAQ59567 Human bra	c 596	17	2.4	606	6	ABH65916	ABH65916 Human can
c 540	17	2.4	434	2	AAQ64812	AAQ64812 Murine FD	c 597	17	2.4	609	6	ABQ34666	ABQ34666 Oligonuc
541	17	2.4	436	4	AA122201	AA122201 Human bre	c 598	17	2.4	609	6	ABQ34667	ABQ34667 Oligonuc
c 542	17	2.4	436	5	ABV34139	ABV34139 Human pro	c 599	17	2.4	616	5	ABV55896	ABV55896 Human pro
543	17	2.4	456	4	AAK88148	AAK88148 Human dig	c 600	17	2.4	618	7	ACA28514	ACA28514 Prokaryot
544	17	2.4	458	5	ABAI3178	ABAI3178 Human ner	c 601	17	2.4	628	6	ABK92464	ABK92464 Human pro
545	17	2.4	462	8	ACH22226	ACH22226 Human adu	c 602	17	2.4	639	2	AB120893	AB120893 Drosophila
546	17	2.4	464	4	AA110630	AA110630 Probe #56	c 603	17	2.4	651	6	ABK35979	ABK35979 CDNA sequ
547	17	2.4	464	4	ABAS2277	ABAS2277 Human foe	c 604	17	2.4	654	7	AB252811	AB252811 Aspergilli
548	17	2.4	464	4	AA131884	AA131884 Probe #57	c 605	17	2.4	660	4	AA104633	AA104633 Human rep
549	17	2.4	464	4	AB22078	AB22078 Probe #54	c 606	17	2.4	660	4	AB197546	AB197546 Human tes
550	17	2.4	464	4	AAK26001	AAK26001 Human bon	c 607	17	2.4	675	2	AAV11700	AAV11700 Bacteriocin
551	17	2.4	464	4	AAK00552	AAK00552 Human bra	c 608	17	2.4	675	2	AAK17724	AAK17724 Bacteriocin
552	17	2.4	464	4	AB25588	AB25588 Human 1lv	c 609	17	2.4	682	6	ABQ44992	ABQ44992 Oligonuc
553	17	2.4	464	4	AA100561	AA100561 Probe #55	c 610	17	2.4	689	5	AAQ00844	AAQ00844 Human cDN
c 554	17	2.4	464	6	AB500582	AB500582 Human gen	c 611	17	2.4	701	3	AAK99940	AAK99940 Human sec
c 555	17	2.4	471	5	ABV13018	ABV13018 Human pro	c 612	17	2.4	712	4	AA123409	AA123409 Human bre
556	17	2.4	486	8	ACH23790	ACH23790 Human adu	c 613	17	2.4	721	6	ABQ79714	ABQ79714 MMV full
c 557	17	2.4	488	4	AA186910	AA186910 Human pol	c 614	17	2.4	727	9	ABD17703	ABD17703 DNA (Seq)
c 558	17	2.4	488	8	ACH27078	ACH27078 Human adu	c 615	17	2.4	728	4	AA162736	AA162736 Human bre
c 559	17	2.4	501	5	ABV60774	ABV60774 Human pro	c 616	17	2.4	728	4	AA107440	AA107440 Human rep
c 560	17	2.4	505	7	ACC60331	ACC60331 R1ce endo	c 617	17	2.4	732	4	AAH88021	AAH88021 Cucumbar
561	17	2.4	505	8	ACH22493	ACH22493 Human adu	c 618	17	2.4	732	4	AA115527	AA115527 Human bre
562	17	2.4	507	5	ABV18201	ABV18201 Human pro	c 619	17	2.4	743	6	ABQ51475	ABQ51475 Oligonuc
c 563	17	2.4	509	4	AA118218	AA118218 Human bre	c 620	17	2.4	743	6	ABQ51476	ABQ51476 Oligonuc
564	17	2.4	522	4	ABA60974	ABA60974 Human foe	c 621	17	2.4	753	3	AAA70190	AAA70190 Plasmodiu
565	17	2.4	522	4	AA140871	AA140871 Probe #95	c 622	17	2.4	760	7	ACF65583	ACF65583 Phototrab
566	17	2.4	522	4	AAK35155	AAK35155 Human bon	c 623	17	2.4	763	4	AAK22943	AAK22943 Human pro
567	17	2.4	522	4	AAK09266	AAK09266 Human bra	c 624	17	2.4	775	8	ACC59728	ACC59728 Nucleotid
568	17	2.4	522	6	AB509597	AB509597 Human gen	c 625	17	2.4	781	4	AA124400	AA124400 Human bre
569	17	2.4	524	6	ABQ44323	ABQ44323 Oligonuc	c 626	17	2.4	790	6	ABQ23800	ABQ23800 Oligonuc
c 570	17	2.4	524	6	ABQ44322	ABQ44322 Oligonuc	c 627	17	2.4	796	6	ABQ23801	ABQ23801 Oligonuc
571	17	2.4	531	9	AD071850	AD071850 Human ur1	c 628	17	2.4	796	6	ABQ41954	ABQ41954 Oligonuc
572	17	2.4	533	7	ACD92635	ACD92635 Human col	c 629	17	2.4	799	3	AAK07810	AAK07810 Fusarium
573	17	2.4	537	4	AAK63362	AAK63362 Human 1mm	c 630	17	2.4	813	4	AA195914	AA195914 Human neu
574	17	2.4	537	6	ABQ21278	ABQ21278 Oligonuc	c 631	17	2.4	819	6	ABQ98941	ABQ98941 Human ORF
c 575	17	2.4	537	6	ABQ21279	ABQ21279 Oligonuc	c 632	17	2.4	821	6	ABK66716	ABK66716 Helicobac
c 576	17	2.4	540	4	AA101003	AA101003 Human rep	c 633	17	2.4				
c 577	17	2.4	540	4	AA101003	AA101003 Human rep	c 634	17	2.4				

c 635	17	2.4	823	5	ABV19757	Abv19757 Human pro	692	17	2.4	1513	2	AA16103	At16103 Xylanase
c 636	17	2.4	830	2	AA162455	At62455 Lambda Sh	693	17	2.4	1542	2	AA142305	At42305 Male-spec
c 637	17	2.4	838	4	AA115741	At115741 Human bre	694	17	2.4	1566	2	AAQ05140	Aeq05140 Sequence
c 638	17	2.4	865	4	AA103440	At03440 Human cDN	695	17	2.4	1628	4	AA533067	Aa533067 DNA encod
c 639	17	2.4	877	4	AA194066	At194066 Human neu	696	17	2.4	1632	6	AAH70417	Ahn70417 Streptococ
c 640	17	2.4	882	6	ABK66545	Abk66545 Helicobac	697	17	2.4	1662	3	AAAC7419	Aac7419 Streptococ
c 641	17	2.4	889	2	AA114390	At114390 H. pylori	698	17	2.4	1662	3	AAAC7419	Aac7419 Streptococ
c 642	17	2.4	909	8	ACCS9705	Accs9705 Acetifida	699	17	2.4	1662	3	AAAC7419	Aac7419 Streptococ
c 643	17	2.4	956	7	AB218441	Ab218441 Group III	700	17	2.4	1665	6	ABK67883	Abk67883 Streptococ
c 644	17	2.4	956	7	AB218441	Ab218441 Group III	701	17	2.4	1680	5	ABV25282	Abv25282 Human pro
c 645	17	2.4	960	7	ACF69120	Accf69120 Photobab	702	17	2.4	1725	2	AAV58270	Aav58270 Zea mays
c 646	17	2.4	988	2	AAQ28117	AAQ28117 P. falcipa	703	17	2.4	1752	7	ACB30329	Ac30329 Streptococ
c 647	17	2.4	1000	8	ADB23168	Adb23168 Envitome	704	17	2.4	1757	7	ABK12157	Abk12157 DNA encod
c 648	17	2.4	1001	3	AAH51776	AAH51776 Human UGT	705	17	2.4	1771	3	AAAI4075	Aai4075 Human SPR
c 649	17	2.4	1001	3	AAH51473	AAH51473 Human UGT	706	17	2.4	1798	3	AAZ49566	Aaz49566 Maize MLO
c 650	17	2.4	1001	3	AAH51475	AAH51475 Human UGT	707	17	2.4	1820	7	ABK33990	Abk33990 Human pig
c 651	17	2.4	1001	3	AAH51474	AAH51474 Human UGT	708	17	2.4	1826	7	ACB21547	Ab21547 Streptococ
c 652	17	2.4	1015	6	ABQ53075	Abq53075 Oligonuc1	709	17	2.4	2000	6	ABK16755	Abk16755 Streptococ
c 653	17	2.4	1015	6	ABQ53074	Abq53074 Oligonuc1	710	17	2.4	2000	6	ABK15957	Abk15957 Streptococ
c 654	17	2.4	1043	3	AAH02498	AAH02498 Human col	711	17	2.4	2000	6	ABK17392	Abk17392 Streptococ
c 655	17	2.4	1080	3	AAK59285	AAK59285 Human sec	712	17	2.4	2030	7	ADK68975	Adk68975 Human SPR
c 656	17	2.4	1095	2	AAK59285	AAK59285 Human sec	713	17	2.4	2048	6	ABK50244	Abk50244 Streptococ
c 657	17	2.4	1095	2	AAK59285	AAK59285 Human sec	714	17	2.4	2048	6	ABK50244	Abk50244 Streptococ
c 658	17	2.4	1095	2	ABK50244	Abk50244 Streptococ	715	17	2.4	2130	7	ABK22523	Abk22523 Streptococ
c 659	17	2.4	1103	2	AAK61382	AAK61382 Human pol	716	17	2.4	2182	5	AAH23831	Aah23831 Streptococ
c 660	17	2.4	1103	2	ADK39831	Adk39831 Human sec	717	17	2.4	2188	9	ABK62780	Abk62780 Human tra
c 661	17	2.4	1103	2	ACB30449	Ac30449 Human sec	718	17	2.4	2194	4	AAI59630	Aai59630 Human cDN
c 662	17	2.4	1103	2	ABK71252	Abk71252 Human sec	719	17	2.4	2214	7	ACB28435	Ab28435 Streptococ
c 663	17	2.4	1103	8	ADK91151	Adk91151 Human sec	720	17	2.4	2226	2	AAV11704	Aav11704 Enterococ
c 664	17	2.4	1103	8	ADK91151	Adk91151 Human sec	721	17	2.4	2226	2	AAV11704	Aav11704 Enterococ
c 665	17	2.4	1106	4	AAI03338	AAI03338 Human rep	722	17	2.4	2227	6	ABK14977	Abk14977 Streptococ
c 666	17	2.4	1113	7	ACB34776	Ac34776 Streptococ	723	17	2.4	2227	6	ABK14977	Abk14977 Streptococ
c 667	17	2.4	1124	6	ABK58163	Abk58163 Human ABC	724	17	2.4	2235	6	ABK67114	Abk67114 Human ang
c 668	17	2.4	1145	2	AAK34089	AAK34089 Streptococ	725	17	2.4	2262	6	ABK69263	Abk69263 Streptococ
c 669	17	2.4	1145	2	AAK34089	AAK34089 Streptococ	726	17	2.4	2262	6	ABK69263	Abk69263 Streptococ
c 670	17	2.4	1155	4	AAK61186	AAK61186 Human imm	727	17	2.4	2282	2	AAV54015	Aav54015 Streptococ
c 671	17	2.4	1155	4	AAK61186	AAK61186 Human imm	728	17	2.4	2282	2	AAV54015	Aav54015 Streptococ
c 672	17	2.4	1158	2	AAV24720	AAV24720 H. pylori	729	17	2.4	2304	4	AAK32646	Aak32646 Streptococ
c 673	17	2.4	1170	7	ACB20688	Ac20688 Streptococ	730	17	2.4	2349	4	AAH43198	Aah43198 Human cDN
c 674	17	2.4	1173	8	ADK32467	Adk32467 DNA encod	731	17	2.4	2349	4	AAH43198	Aah43198 Human cDN
c 675	17	2.4	1176	4	AAK53791	AAK53791 Helicobac	732	17	2.4	2393	4	AAI57844	Aai57844 Human ger
c 676	17	2.4	1188	5	AAH41136	AAH41136 Streptococ	733	17	2.4	2396	4	ABK04156	Abk04156 Streptococ
c 677	17	2.4	1201	3	AAK62524	AAK62524 Human sec	734	17	2.4	2466	9	ABK43917	Abk43917 Streptococ
c 678	17	2.4	1201	3	AAK62524	AAK62524 Human sec	735	17	2.4	2466	9	ABK43917	Abk43917 Streptococ
c 679	17	2.4	1254	7	ACB23020	Ac23020 Streptococ	736	17	2.4	2474	2	AAV90771	Aav90771 Streptococ
c 680	17	2.4	1259	3	AAK66428	AAK66428 Human sec	737	17	2.4	2542	6	ABK90868	Abk90868 Streptococ
c 681	17	2.4	1275	7	ACB21616	Ac21616 Streptococ	738	17	2.4	2545	2	AAQ04645	Aaq04645 Rat memb
c 682	17	2.4	1282	2	AAQ29958	AAQ29958 5-Substf.	739	17	2.4	2545	2	AAQ04645	Aaq04645 Rat memb
c 683	17	2.4	1320	2	AAQ80916	AAQ80916 Plasmodu	740	17	2.4	2545	2	AAQ04645	Aaq04645 Rat memb
c 684	17	2.4	1320	2	AAQ80916	AAQ80916 Plasmodu	741	17	2.4	2545	2	AAQ04645	Aaq04645 Rat memb
c 685	17	2.4	1320	2	AAQ80916	AAQ80916 Plasmodu	742	17	2.4	2545	2	AAQ04645	Aaq04645 Rat memb
c 686	17	2.4	1323	2	AAV72050	AAV72050 Sequence	743	17	2.4	2670	7	ACB33101	Ab33101 Streptococ
c 687	17	2.4	1350	2	AAV90860	AAV90860 Nucleotid	744	17	2.4	2723	9	ADK38734	Adk38734 Streptococ
c 688	17	2.4	1364	5	AAK64383	AAK64383 DNA encod	745	17	2.4	2743	4	ABK20310	Abk20310 Streptococ
c 689	17	2.4	1407	6	ABK56226	Abk56226 Streptococ	746	17	2.4	2751	2	AAK30434	Aak30434 Streptococ
c 690	17	2.4	1427	6	AAK73067	AAK73067 Human imm	747	17	2.4	2781	4	AAH73960	Aah73960 Human hel
c 691	17	2.4	1493	9	ADK50713	Adk50713 Streptococ	748	17	2.4	2814	6	ABK34126	Abk34126 Streptococ

c 749	17	2.4	2829	3	AAc90465	Human unc	806	17	2.4	4574	4	ABL16449	ABL16449
c 750	17	2.4	2835	2	AAx91639	Porphrym	c 807	17	2.4	4619	4	ABL01968	ABL101968
c 751	17	2.4	2912	7	ACC48536	Stephyloc	c 808	17	2.4	4623	4	ABL12280	ABL112280
c 752	17	2.4	2937	7	ACc30450	Prokaryot	c 809	17	2.4	4623	4	ABL20892	ABL20892
c 753	17	2.4	2964	4	AAFB8022	Cucumber	c 810	17	2.4	4762	3	AAZ36710	AAZ36710
c 754	17	2.4	2964	7	ABX13453	C. sativu	c 811	17	2.4	4772	7	ACC50330	ACC50330
c 755	17	2.4	2984	4	ABL30152	Drosophill	c 812	17	2.4	4826	4	ABL18252	ABL18252
c 756	17	2.4	2990	2	AAQ04123	Adenyl cy	c 813	17	2.4	4826	4	ABL12278	ABL12278
c 757	17	2.4	3001	3	AAH51771	Chromosom	c 814	17	2.4	4954	4	AAK74818	AAK74818
c 758	17	2.4	3001	6	ABN84406	Human sup	c 815	17	2.4	4959	6	ABV99146	ABV99146
c 759	17	2.4	3030	7	ABE210166	Abz10166	c 816	17	2.4	4980	4	ABL03516	ABL03516
c 760	17	2.4	3030	7	ABE210020	Abz10020	c 817	17	2.4	5032	6	AA561083	AA561083
c 761	17	2.4	3037	6	ABK33994	Human DNA	c 818	17	2.4	5033	6	AA546373	AA546373
c 762	17	2.4	3037	7	ADN20424	Prostate	c 819	17	2.4	5072	2	AAx34633	AAx34633
c 763	17	2.4	3037	7	ADN4231	Human ren	c 820	17	2.4	5102	6	ABL92274	ABL92274
c 764	17	2.4	3041	4	ABL11656	Abk11656	c 821	17	2.4	5126	6	ABL70493	ABL70493
c 765	17	2.4	3063	6	ABK84249	Abk84249	c 822	17	2.4	5133	6	ABL33913	ABL33913
c 766	17	2.4	3077	7	ABE210216	Abz10216	c 823	17	2.4	5164	6	ABO67122	ABO67122
c 767	17	2.4	3105	4	ABL15038	Ab115038	c 824	17	2.4	5179	6	ABL33996	ABL33996
c 768	17	2.4	3148	4	ABL11120	Ab111120	c 825	17	2.4	5179	6	ABL32826	ABL32826
c 769	17	2.4	3203	4	ABL11156	Ab111156	c 826	17	2.4	5187	9	ADB67038	ADB67038
c 770	17	2.4	3298	6	ABK93938	Abk93938	c 827	17	2.4	5219	6	ABL32768	ABL32768
c 771	17	2.4	3304	4	ABL16584	Ab116584	c 828	17	2.4	5261	6	ABL70577	ABL70577
c 772	17	2.4	3416	4	ABL16580	Ab116580	c 829	17	2.4	5261	6	AA561392	AA561392
c 773	17	2.4	3505	2	AAx84667	AAx84667	c 830	17	2.4	5276	6	AA546376	AA546376
c 774	17	2.4	3520	4	AAH54185	AAH54185	c 831	17	2.4	5276	6	ABL32826	ABL32826
c 775	17	2.4	3674	4	ABL29836	Ab129836	c 832	17	2.4	5283	6	ABL33893	ABL33893
c 776	17	2.4	3689	4	AAH29914	AAH29914	c 833	17	2.4	5312	7	ADA20357	ADA20357
c 777	17	2.4	3714	7	ACA28933	ACA28933	c 834	17	2.4	5312	7	ADN84164	ADN84164
c 778	17	2.4	3750	4	ABL02680	Ab102680	c 835	17	2.4	5312	9	ADB54090	ADB54090
c 779	17	2.4	3775	6	ABQ70853	Abq70853	c 836	17	2.4	5312	9	ADB54218	ADB54218
c 780	17	2.4	3830	7	ABK69844	Abk69844	c 837	17	2.4	5312	9	ADB54080	ADB54080
c 781	17	2.4	3830	7	ADN57726	ADN57726	c 838	17	2.4	5312	9	ADB54156	ADB54156
c 782	17	2.4	3830	7	ACCS0859	ACCS0859	c 839	17	2.4	5325	3	AAA58001	AAA58001
c 783	17	2.4	3830	8	ADB91837	ADB91837	c 840	17	2.4	5397	6	ABL33044	ABL33044
c 784	17	2.4	3830	9	ADC74612	ADC74612	c 841	17	2.4	5397	6	ABL32142	ABL32142
c 785	17	2.4	3830	9	ADD38132	ADD38132	c 842	17	2.4	5397	6	ABL31463	ABL31463
c 786	17	2.4	3844	6	ABK69847	Abk69847	c 843	17	2.4	5407	6	AA561379	AA561379
c 787	17	2.4	3844	7	ADN57729	ADN57729	c 844	17	2.4	5407	6	AA561379	AA561379
c 788	17	2.4	3844	7	ACCS0862	ACCS0862	c 845	17	2.4	5432	6	AA561379	AA561379
c 789	17	2.4	3844	7	ABE211484	ABE211484	c 846	17	2.4	5432	6	AA561379	AA561379
c 790	17	2.4	3844	8	ADB91840	ADB91840	c 847	17	2.4	5452	6	ABL33149	ABL33149
c 791	17	2.4	3844	8	ADC74615	ADC74615	c 848	17	2.4	5452	6	ABL33905	ABL33905
c 792	17	2.4	3844	9	ADD38135	ADD38135	c 849	17	2.4	5508	6	ABL33130	ABL33130
c 793	17	2.4	3844	9	ABD30538	ABD30538	c 850	17	2.4	5514	6	ABL33262	ABL33262
c 794	17	2.4	3878	2	AAV31377	AAV31377	c 851	17	2.4	5537	2	AAQ90330	AAQ90330
c 795	17	2.4	3956	2	ABK91986	Abk91986	c 852	17	2.4	5537	2	AAQ90330	AAQ90330
c 796	17	2.4	4043	6	ABK91986	Abk91986	c 853	17	2.4	5537	2	AAQ90330	AAQ90330
c 797	17	2.4	4063	4	ABL28494	ABL28494	c 854	17	2.4	5546	6	ABL32390	ABL32390
c 798	17	2.4	4244	3	AA69145	AA69145	c 855	17	2.4	5546	6	ABL34004	ABL34004
c 799	17	2.4	4253	3	AAH18524	AAH18524	c 856	17	2.4	5557	6	ABL33546	ABL33546
c 800	17	2.4	4286	3	AAO9207	AAO9207	c 857	17	2.4	5565	6	ABL32262	ABL32262
c 801	17	2.4	4445	4	ABL16443	ABL16443	c 858	17	2.4	5649	6	AA546384	AA546384
c 802	17	2.4	4446	4	ABK42730	ABK42730	c 859	17	2.4	5649	6	ABK40008	ABK40008
c 803	17	2.4	4446	8	ADB60886	ADB60886	c 860	17	2.4	5649	6	ABL32849	ABL32849
c 804	17	2.4	4501	4	ABL10480	ABL10480	c 861	17	2.4	5649	9	ADB54126	ADB54126
c 805	17	2.4	4537	4	ABL12154	ABL12154	c 862	17	2.4	5649	9	ADB54254	ADB54254

c 863	17	2.4	5649	9	AD684108	Human	Lym	c 920	17	2.4	6102	6	AB133496	Ab133496	Human	Imm
c 864	17	2.4	5649	9	AD684184	Human	Lym	c 921	17	2.4	6103	6	AB133691	Ab133691	Human	Imm
c 865	17	2.4	5690	6	ABK40027	Human	Che	c 922	17	2.4	6107	6	ABN80104	Abn80104	Human	Che
c 866	17	2.4	5690	6	AB133324	Human	Imm	c 923	17	2.4	6121	6	AB133975	Ab133975	Human	Imm
c 867	17	2.4	5690	6	AA663330	Chemical		c 924	17	2.4	6132	6	AB133990	Ab133990	Human	Imm
c 868	17	2.4	5695	6	AA546537	Human	Imm	c 925	17	2.4	6184	6	AB133253	Ab133253	Human	Imm
c 869	17	2.4	5702	9	AD631422	Human	Imm	c 926	17	2.4	6184	6	AB133456	Ab133456	Human	Imm
c 870	17	2.4	5736	4	AD631422	Human	Imm	c 927	17	2.4	6215	6	AB133190	Ab133190	Human	Imm
c 871	17	2.4	5736	4	AD631422	Human	Imm	c 928	17	2.4	6216	6	AB133932	Ab133932	Human	Imm
c 872	17	2.4	5736	4	AD631422	Human	Imm	c 929	17	2.4	6216	6	AB170139	Ab170139	Human	Che
c 873	17	2.4	5736	4	AD631422	Human	Imm	c 930	17	2.4	6233	6	AA546497	AA546497	Human	Imm
c 874	17	2.4	5763	6	AB133289	Human	Imm	c 931	17	2.4	6239	6	ABK93553	ABK93553	Human	Imm
c 875	17	2.4	5763	6	AB133289	Human	Imm	c 932	17	2.4	6247	6	AB133275	AB133275	Human	Imm
c 876	17	2.4	5776	6	AB133289	Human	Imm	c 933	17	2.4	6255	6	AB134028	AB134028	Human	Imm
c 877	17	2.4	5776	6	AB133289	Human	Imm	c 934	17	2.4	6271	6	AA546455	AA546455	Human	Imm
c 878	17	2.4	5786	5	AB133289	Human	Imm	c 935	17	2.4	6271	6	AB133336	AB133336	Human	Imm
c 879	17	2.4	5786	5	AB133289	Human	Imm	c 936	17	2.4	6271	6	AB133977	AB133977	Human	Imm
c 880	17	2.4	5814	6	AB133560	Human	Imm	c 937	17	2.4	6271	7	AD620370	AD620370	Human	Imm
c 881	17	2.4	5829	6	AB133727	Human	Imm	c 938	17	2.4	6271	7	AD684177	AD684177	Human	Imm
c 882	17	2.4	5883	6	AB133253	Human	Imm	c 939	17	2.4	6299	6	AB115032	AB115032	Human	Imm
c 883	17	2.4	5883	6	AB134473	Human	Imm	c 940	17	2.4	6309	6	AB132304	AB132304	Human	Imm
c 884	17	2.4	5891	6	AB133439	Human	Imm	c 941	17	2.4	6348	7	ACF65364	ACF65364	Human	Imm
c 885	17	2.4	5917	6	ABK31469	Human	Imm	c 942	17	2.4	6350	6	AB134628	AB134628	Human	Imm
c 886	17	2.4	5921	6	AA546656	Human	Imm	c 943	17	2.4	6350	6	AB170499	AB170499	Human	Imm
c 887	17	2.4	5921	6	AB133361	Human	Imm	c 944	17	2.4	6352	6	AB132905	AB132905	Human	Imm
c 888	17	2.4	5938	6	ABN80219	Human	Imm	c 945	17	2.4	6352	7	AD620359	AD620359	Human	Imm
c 889	17	2.4	5952	9	AD654319	Human	Imm	c 946	17	2.4	6352	7	AD684166	AD684166	Human	Imm
c 890	17	2.4	5952	9	AD654319	Human	Imm	c 947	17	2.4	6365	6	AB132124	AB132124	Human	Imm
c 891	17	2.4	5989	6	AB170287	Chemical		c 948	17	2.4	6397	6	AB132819	AB132819	Human	Imm
c 892	17	2.4	5989	6	AA561212	Human	Imm	c 949	17	2.4	6459	7	AB279546	AB279546	Human	Imm
c 893	17	2.4	5989	6	AB154351	Chemical		c 950	17	2.4	6461	4	AA531467	AA531467	Human	Imm
c 894	17	2.4	5992	6	AA561208	Human	Imm	c 951	17	2.4	6461	4	AA531467	AA531467	Human	Imm
c 895	17	2.4	5992	6	AA561208	Human	Imm	c 952	17	2.4	6461	9	AD611078	AD611078	Human	Imm
c 896	17	2.4	5999	6	ABK39961	Human	Imm	c 953	17	2.4	6470	6	ABQ67091	ABQ67091	Human	Imm
c 897	17	2.4	5999	6	ABK39961	Human	Imm	c 954	17	2.4	6500	6	AB133200	AB133200	Human	Imm
c 898	17	2.4	6012	4	AA546724	Human	Imm	c 955	17	2.4	6503	6	AB132721	AB132721	Human	Imm
c 899	17	2.4	6013	4	AA563314	Human	Imm	c 956	17	2.4	6509	6	ABK31189	ABK31189	Human	Imm
c 900	17	2.4	6031	4	AA546621	Human	Imm	c 957	17	2.4	6509	6	AA561086	AA561086	Human	Imm
c 901	17	2.4	6035	6	AB133525	Human	Imm	c 958	17	2.4	6521	9	AD654141	AD654141	Human	Imm
c 902	17	2.4	6041	4	AB127104	Drosophila		c 959	17	2.4	6535	4	AA546470	AA546470	Human	Imm
c 903	17	2.4	6042	6	AB133592	Human	Imm	c 960	17	2.4	6552	6	ABN80141	ABN80141	Human	Imm
c 904	17	2.4	6047	6	AB133459	Human	Imm	c 961	17	2.4	6577	6	AB133357	AB133357	Human	Imm
c 905	17	2.4	6048	4	AA546614	Tumour	su	c 962	17	2.4	6577	6	AB170562	AB170562	Chemical	
c 906	17	2.4	6059	6	AB133481	Human	Imm	c 963	17	2.4	6577	6	AA561222	AA561222	Human	Imm
c 907	17	2.4	6059	6	AB133480	Human	Imm	c 964	17	2.4	6608	6	AB134035	AB134035	Human	Imm
c 908	17	2.4	6059	6	AB134343	Chemical		c 965	17	2.4	6624	6	AB132043	AB132043	Human	Imm
c 909	17	2.4	6070	6	AB132241	Human	Imm	c 966	17	2.4	6641	6	AB132315	AB132315	Human	Imm
c 910	17	2.4	6070	6	AB192199	Chemical		c 967	17	2.4	6641	6	AB154336	AB154336	Human	Imm
c 911	17	2.4	6070	6	AB149310	Human	Imm	c 968	17	2.4	6712	6	AB132691	AB132691	Human	Imm
c 912	17	2.4	6073	6	AB133543	Human	Imm	c 969	17	2.4	6731	6	AB133061	AB133061	Human	Imm
c 913	17	2.4	6074	6	AB133065	Human	Imm	c 970	17	2.4	6782	6	AB132776	AB132776	Human	Imm
c 914	17	2.4	6074	6	ABN95880	Gene	#237	c 971	17	2.4	6800	4	AA546640	AA546640	Human	Imm
c 915	17	2.4	6077	9	AD654296	Human	Imm	c 972	17	2.4	6800	6	ABN80253	ABN80253	Human	Imm
c 916	17	2.4	6077	9	AD654296	Human	Imm	c 973	17	2.4	6811	6	AB134540	AB134540	Human	Imm
c 917	17	2.4	6081	6	AB133429	Human	Imm	c 974	17	2.4	6811	6	AB170263	AB170263	Chemical	
c 918	17	2.4	6081	6	ABN80193	Human	Imm	c 975	17	2.4	6831	6	AB133487	AB133487	Human	Imm
c 919	17	2.4	6096	4	AB109666	Drosophila		c 976	17	2.4	6842	4	AB112114	AB112114	Drosophila	

QY 361 CAAATATATTCAGCTATATTAAAGAGTTTCATTAATAATACAAAAACAAACACA 420
DB 361 CAAATATATTCAGCTATATTAAAGAGTTTCATTAATAATACAAAAACAAACACA 420
QY 421 GAATTCATCACTAAGAGTATTTTATGAAATTAATGATGATGATGATGATGATGAT 480
DB 421 GAATTCATCACTAAGAGTATTTTATGAAATTAATGATGATGATGATGATGATGAT 480
QY 481 AAATTAATTAATTAATGACAGAAACATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 481 AAATTAATTAATTAATGACAGAAACATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 541 AAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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QY 601 ATTAAGAAAGTTTACCCCAAAAAATTAATAATTAATTAATTAATTAATTAATTAATTA 660
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QY 661 TTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 714
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RESULT 2
AA68247/c
ID AA68247 standard; DNA; 41708 BP.

XX AAA68247;
AC
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS *Staphylococcus aureus*; bacteriophage 77.
PN WO200032825-A2.
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WC-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGE TECH INC.

PI Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Example 3; Page 141-151; 456pp; English.

CC The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA68243 to AA69442 and AB16923 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 714; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 9.5e-300;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 60
DB 23982 ATGAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 23923
QY 61 AAAAGTTAGTTCAGATATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
DB 23922 AAAAGTTAGTTCAGATATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 23863
QY 121 AAAAGTTTATTCAGATATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
DB 23862 AAAAGTTTATTCAGATATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 23803
QY 181 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 23802 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 23743
QY 241 ACGAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
DB 23742 ACGAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 23683
QY 301 ATGATTTGATTTGAAATGAGATATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
DB 23682 ATGATTTGATTTGAAATGAGATATTAATTAATTAATTAATTAATTAATTAATTAAT 23623
QY 361 CAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
DB 23622 CAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23563
QY 421 GAATTCATCACTAAGAGTATTTTATGAAATTAATGATGATGATGATGATGATGATGAT 480

Db 23562 GAAATTCATCACTAAAGATTAATTTATGAAATTAATCTGATAGTTAGAAATGAAAT 23503
Qy 481 AATTAATTAATTAATGACAGAAACATTAATTAATGATAGTACGATGATAGTAA 540
Db 23502 AATTAATTAATTAATGACAGAAACATTAATTAATGATAGTACGATGATAGTAA 23443
Qy 541 AATTAATTAATTAATGATAGTACGATGATAGTACGATGATAGTAA 600
Db 23442 AATTAATTAATTAATGATAGTACGATGATAGTACGATGATAGTAA 23383
Qy 601 AATTAATTAATTAATGATAGTACGATGATAGTACGATGATAGTAA 660
Db 23382 AATTAATTAATTAATGATAGTACGATGATAGTACGATGATAGTAA 23323
Qy 661 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 714
Db 23322 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23269

RESULT 3
AAC86106/c
ID AAC86106 standard; cDNA; 41708 BP.
XX
AC AAC86106;
XX
XX 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
XX Complete genome of bacteriophage 77.
DE
XX DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW screening assay; ss.
XX
XX Bacteriophage.
OS
XX WO200146383-A2.
PN
XX 28-JUN-2001.
PD
XX
XX 21-DEC-2000; 2000MO-US035180.
PF
XX 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689952.
XX
XX (PHAG-) PHAGE TECH INC.
PA (WILL/) WILLIAMS K M.
XX
XX Polioletor J, Gros P, Dubow M;
PI
XX WPI; 2001-418052/44.
DR
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by *Staphylococcus*
PT aureus.
XX
PS Disclosure; Fig 2; 107pp; English.

XX This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially *Staphylococcus*, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 714; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 9.5e-300;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
Db 23982 ATGACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23923
Qy 61 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 23922 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23863
Qy 121 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
Db 23862 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23803
Qy 181 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 23802 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23743
Qy 241 ACGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
Db 23742 ACGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23683
Qy 301 ATGAATTTGATTTGAAATGGAATGATTAATTAATTAATTAATTAATTAATTAAT 360
Db 23682 ATGAATTTGATTTGAAATGGAATGATTAATTAATTAATTAATTAATTAATTAAT 23623
Qy 361 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Db 23622 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23563
Qy 421 GAATTCATCACTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Db 23562 GAATTCATCACTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23503
Qy 481 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Db 23502 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23443
Qy 541 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Db 23442 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 23383

QY 601 ATAGAGAAAGTTTACCCCAAAATTAATCAAGTATAGATTCTCCGATATTATG 660
 DB 23382 ATAGAGAAAGTTTACCCCAAAATTAATCAAGTATAGATTCTCCGATATTATG 23323
 QY 661 TTACTGATTAATAGATTAAATTAATTAATTCAGATCCCTGATTAAGATGA 714
 DB 23322 TTACTGATTAATAGATTAAATTAATTAATTCAGATCCCTGATTAAGATGA 23289

RESULT 4
 ABQ30760/c
 ID ABQ30760 standard; DNA; 656 BP.
 AC ABQ30760;
 DT 12-JUL-2002 (first entry)
 XX
 DE oligonucleotide for detecting cytosine methylation SEQ ID NO 17351.
 KW Human; cytosine methylation; 5'-OpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 PR 03-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Pienbrock C, Berlin K, Guetig D;
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56bp + Sequence Listing; 56bp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-OpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert in a
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:

CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ34121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

SEQ Sequence 656 BP; 72 A; 69 C; 242 G; 273 T; 0 U; 0 Other;
 Query Match 3.2%; Score 23; DB 6; Length 656;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 TTGGATTAATTAATTCACAAAATA 413
 DB 580 TTGGATTAATTAATTCACAAAATA 558

RESULT 5
 ABQ30761
 ID ABQ30761 standard; DNA; 656 BP.
 AC ABQ30761;
 DT 12-JUL-2002 (first entry)
 XX
 DE oligonucleotide for detecting cytosine methylation SEQ ID NO 17352.
 KW Human; cytosine methylation; 5'-OpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 PR 03-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Pienbrock C, Berlin K, Guetig D;
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (11) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 656 BP; 273 A; 242 C; 69 G; 72 T; 0 U; 0 Other;
Query Match 3.2%; Score 23; DB 6; Length 656;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 391 TTCGATAAAAATACCAAAAAA 413
DB 77 TTCGATAAAAATACCAAAAAA 99
RESULT 6
ABQ38659
ID ABQ38659 standard; DNA; 712 BP.
XX
AC ABQ38659;
XX
DT 12-JUL-2002 (first entry)
XX
DE oligonucleotide for detecting cytosine methylation SEQ ID NO 25250.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-BP010074.

XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guettig D;
XX WPI; 2002-371829/40.
DR
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (11) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 712 BP; 274 A; 276 C; 80 G; 82 T; 0 U; 0 Other;
Query Match 3.2%; Score 23; DB 6; Length 712;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 391 TTCGATAAAAATACCAAAAAA 413
DB 167 TTCGATAAAAATACCAAAAAA 189
RESULT 7
ABQ38658/c
ID ABQ38658 standard; DNA; 712 BP.
XX
AC ABQ38658;
XX
DT 12-JUL-2002 (first entry)
XX
DE oligonucleotide for detecting cytosine methylation SEQ ID NO 25249.

XX Human; cytosine methylation; 5'-O⁶-G-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 PR 03-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guettig D;
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-O⁶-G-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert in a
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (11) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 XX
 SQ Sequence 712 BP; 82 A; 80 C; 276 G; 274 T; 0 U; 0 Other;
 Query Match 3.2%; Score 23; DB 6; Length 712;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 546 TTAGATAAAAATACCAAAAAA 524
 RESULT 8
 ABL33621
 ID ABL33621 standard; DNA; 6254 BP.
 XX
 AC ABL33621;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 1594.
 XX
 KW Human; immune system disease; cytosine methylation; antileukemic;
 KW antileukocytocytic; antileukemic; cytosine; neoplastic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antileukemic; antileukemic; antidiabetic; antipsychotic;
 KW antileukemic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007537.
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX
 PS Claim 1; SEQ ID NO 1594; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX
 SQ Sequence 6254 BP; 1867 A; 44 C; 1323 G; 3020 T; 0 U; 0 Other;

Query Match 3.2%; Score 23; DB 6; Length 6254;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 328 TATTTAAGATGTTTAAATTT 350
|||||
DB 957 TATTTAAGATGTTTAAATTT 979

RESULT 9
ABL33550
ID ABL33550 standard; DNA; 6075 BP.

AC ABL33550;
XX 26-MAR-2002 (first entry)
XX Human immune system associated gene SEQ ID NO: 1523.

DE Human immune system associated gene SEQ ID NO: 1523.
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antiamebic; cytosine; neutrotic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antitubercular; antileishmanic; antidiabetic; antiparasitic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW dr.

OS Homo sapiens.
XX WO200200928-A2.
PN 03-JAN-2002.

PD 02-JUL-2001; 2001WO-EP007537.
XX 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130909/17.

DR Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX Claim 1; SEQ ID NO 1523; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX SQ Sequence 6075 BP; 1318 A; 146 C; 1645 G; 2966 T; 0 U; 0 Other;

Query Match 3.1%; Score 22; DB 6; Length 6075;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 ATTGATAGGTAAAAAATTAA 547
|||||
DB 2292 ATTGATAGGTAAAAAATTAA 2313

RESULT 10
AAA4336/c
ID AAA4336 standard; cDNA; 615 BP.

AC AAA4336;
XX 21-AUG-2000 (first entry)
XX Xenopus secreted expressed sequence tag SEQ ID NO: 2076.

DE Xenopus secreted expressed sequence tag SEQ ID NO: 2076.
XX Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;
KW thrombolytic; antineoplastic; cytosine; antibacterial; antifungal;
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparasitic;
KW antitumor; osteopathic; neuroprotective; neutrotic; antiparasitic;
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
KW autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW hemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
KW infection; depression; psoriasis; ss.

OS Xenopus sp.
XX WO200021990-A1.
PN 20-APR-2000.

PD 15-OCT-1999; 99WO-US024205.
XX 15-OCT-1998; 98US-0104435P.
PR (GENE) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallee ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M;
XX WPI; 2000-317937/27.
DR Isolated polynucleotides, and encoded proteins, comprising secreted

PT expressed sequence tags (ESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders.
 XX
 PS Claim 1; Page 594; 618pp; English.
 XX
 CC AAA41261 to AAA43419 represent specifically claimed secreted expressed
 CC sequence tags (ESTs), isolated from human, mouse, xenopus and rat tissue
 CC sources. The ESTs can have a range of activities depending on the
 CC tissues they were isolated from. The activities include: chemotactic;
 CC proliferative; immunomodulatory; haematopoietic; chemokine; analgesic;
 CC haemostatic; thrombolytic; anti-inflammatory; cytostatic; antibacterial;
 CC antifungal; antiviral; antidiabetic; antisthmatic; vulnary; antitumor;
 CC osteoprotective; neuroprotective; nootropic; antiparkinsonian; antipruritic;
 CC cerebroprotective; anticonvulsant; and antidepressant. The ESTs can be
 CC used for gene therapy and in vaccines. The ESTs are useful as probes for
 CC the identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the ESTs. Proteins encoded by the ESTs
 CC are useful in assays for determining biological activity and relating
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease, tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 615 BP; 142 A; 127 C; 130 G; 216 T; 0 U; 0 Other;
 Query Match 2.9%; Score 21; DB 3; Length 615;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 407 AAAAAAAAAACACAGAAATCA 427
 Db 400 AAAAAAAAAACACAGAAATCA 380
 RESULT 11
 AB216393
 ID AB216393 standard; DNA; 2000 BP.
 XX
 AC AB216393;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4198.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W0200216655-A2.
 XX
 PD 28-FEB-2002.
 XX

PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 PS Claim 144; SEQ ID NO 4198; 577bp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 2000 BP; 718 A; 262 C; 272 G; 748 T; 0 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 475 GAAATTAATTAATTAATTAAT 495
 Db 48 GAAATTAATTAATTAATTAAT 68
 RESULT 12
 AAT90505
 ID AAT90505 standard; DNA; 5156 BP.
 XX
 AC AAT90505;
 XX
 DT 17-OCT-2003 (revised)
 XX
 DT 29-JAN-1998 (first entry)
 XX
 DE Arabidopsis thaliana ferulate-5-hydroxylase genomic DNA.
 XX
 KW Ferulate-5-hydroxylase; lignin; delignification; pulp; paper; feedstock;
 KW transgenic plant; alfalfa; Medicago; rice; Oryza; maize; Zea mays;
 KW oilseed rape; Brassica; forage grass; fabi gene; tobacco; Nicotiana;
 KW eucalyptus; pine; Pinus; spruce; Picea; poplar; Populus;
 XX

KW crop improvement; Arabidopsis thaliana; ss.
 OS Arabidopsis thaliana; ecotype Landsberg erecta.
 XX
 FH Key Location/Qualifiers
 FT exon 2487..3002 /tag= b
 FT /number= 1
 FT CDS 2587..4522 /tag= a
 FT /note= "includes introns"
 FT Intron 3003..3130 /tag= c
 FT /number= 1
 FT exon 3131..3557 /tag= d
 FT /number= 2
 FT Intron 3558..3902 /tag= e
 FT /number= 2
 FT exon 3903..4522 /tag= f
 FT /number= 3
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 PN WO9723599-A2.
 XX
 PD 03-JUL-1997.
 XX
 PF 19-DEC-1996; 96WO-US020094.
 XX
 PR 22-DEC-1995; 95US-0009119P.
 PR 14-MAR-1996; 96US-0013388P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PA (PURD) PURDUE RES FOUND.
 XX
 PI Chapple C;
 XX
 DR WPI: 1997-351042/32.
 DR P-PSDB; AAW26640.
 XX
 XX
 PT Nucleic acid encoding plant ferulate-5-hydroxylase - useful for altering
 PT galactyl:syringyl lignin monomer ratio in plants, to increase chemical
 PT delignification in paper and pulp making or to increase digestibility of
 PT feedstocks.
 XX
 PS Claim 2; Page 29-31; 43pp; English.
 XX
 CC This genomic DNA sequence includes exons that encode the ferulate-5-
 CC hydroxylase (F5H) (see AAW26640) of Arabidopsis thaliana. It comprises a
 CC HindIII-XhoI fragment of genomic clone pBIC20-F5H, which was isolated
 CC from a genomic library generated in binary cosmid vector pBIC20 by
 CC screening with a F5H cDNA insert (see AAT90504). A claimed chimeric gene
 CC that causes an altered galactyl:syringyl lignin monomer ratio in a
 CC transformed plant comprises the F5H cDNA or genomic clone linked either
 CC in the sense or antisense direction to at least one regulatory sequence.
 CC The gene allows the alteration of a plant's lignin content, especially to

CC increase the syringyl lignin content. This renders the lignin more
 CC susceptible to chemical delignification of use to the paper and pulp
 CC industries. Alteration of the lignin content of grasses increases the
 CC digestibility for animal feedstocks. Suitable host plants include
 CC alfalfa, rice, maize, oilseed rape, forage grasses, tobacco, and tree
 CC crops such as eucalyptus, pine, spruce and poplar. (Updated on 17-OCT-2003
 CC to standardise os field)
 XX
 SQ Sequence 5156 BP; 1670 A; 827 C; 907 G; 1752 T; 0 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 475 GAAATTAATTAAATTAATT 495
 DB 537 GAAATTAATTAAATTAATT 557
 RESULT 13
 AAV10238
 ID AAV10238 standard; cDNA; 5156 BP.
 AC AAV10238;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Arabidopsis ferulate-5-hydroxylase genomic DNA.
 XX
 KW Ferulate-5-hydroxylase; cinnamate-4-hydroxylase;
 KW tissue-specific promoter; lignin; syringyl; delignification; pulping;
 KW transgenic plant; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
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 FT /number= 2
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 XX
 PN WO9803535-A1.
 XX
 PD 29-JAN-1998.
 XX
 PF 18-JUL-1997; 97WO-US012624.
 XX
 PR 19-JUL-1996; 96US-0022228P.
 PR 16-DEC-1996; 96US-0032908P.
 XX
 PA (PURD) PURDUE RES FOUND.
 XX

PI Chapple CCS;
 XX
 DR WPI; 1998-120689/11.
 DR P-PSDB; AAW40099.
 XX
 XX Tissue-specific regulatory plant promoter linked to ferulate-5-
 PT hydroxylase gene - useful for manipulation of plant lignin composition.
 XX
 ES Claim 14; Page 48-51; 71pp; English.
 XX
 CC This genomic DNA sequence includes a coding region, interrupted by 2
 CC introns, that codes for the ferulate-5-hydroxylase (FSH, see AAW40099) of
 CC Arabidopsis thaliana. It comprises the HindIII-XhoI fragment of pBIC20-
 CC FSH genomic clone isolated from a pBIC30 cosmid library using FSH cDNA
 CC (see AAV10237) as probe. FSH is a cytochrome P450-dependent monooxygenase
 CC that catalyzes the meta-hydroxylation of ferulic acid in the monomer-
 CC specific pathway branch required for sinapic acid and syringyl lignin
 CC biosynthesis. A tissue-specific regulatory plant promoter, preferably
 CC derived from the regulatory region of the C4H gene (see AAV10236) can be
 CC linked to the FSH gene in order to increase the syringyl content of
 CC lignin in a transformed plant such as alfalfa, rice, maize, oilseed rape,
 CC forage grasses, eucalyptus, pine, spruce, poplar, Arabidopsis and
 CC tobacco. Increased levels of syringyl monomer residues in lignin renders
 CC the polymer more readily delignified so that the plant is more readily
 CC pulped or digested
 XX
 SQ Sequence 5156 BP; 1671 A; 827 C; 906 G; 1752 T; 0 U; 0 Other;
 Query Match 2.9%; Score 21; DB 2; Length 5156;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 475 GAAATTAATTAATTAATTT 495
 DB 537 GAAATTAATTAATTAATTT 557

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 FT exon 3131. .3536
 FT /*tag= d
 FT /number= 2
 FT Intron 3557. .3901
 FT /*tag= e
 FT exon /number= 2
 FT 3902. .4519
 FT /*tag= f
 FT /number= 3
 PD WO200046382-A1.
 XX 10-AUG-2000.
 XX 31-JAN-2000; 2000WO-CA000074.
 XX 01-FEB-1999; 99US-0118124P.
 XX (SILV-) SILVAGEN INC.
 XX Ellis DD, Chapple CCS, Gilbert M;
 DR WPI; 2000-524419/47.
 DR P-PSDB; AAB15188.
 XX
 XX Producing a transformed gymnosperm plant or precursor containing an
 PT expressible transgene for modifying the lignin composition in the plant,
 PT comprises gene transfer into cells and regeneration of the plant or
 PT precursor.
 XX
 XX Disclosure; Fig 4; 33pp; English.
 XX The present sequence is the Arabidopsis ferulate 5-hydroxylase (FSH)
 CC gene. FSH is an important enzyme for the biosynthesis of lignin. This
 CC gene may be introduced into gymnosperm plants to produce transgenic
 CC plants to result in modification of the lignin composition in the
 CC transgenic plant compared to an average lignin composition of
 CC untransformed wild type plants. The transgenic plants with modified
 CC lignin compositions would be more commercially desirable, since lignin
 CC needs to be removed during chemical pulping and therefore the cost of the
 CC removal of lignin from fibres is reduced
 XX
 SQ Sequence 5156 BP; 1670 A; 827 C; 907 G; 1752 T; 0 U; 0 Other;
 Query Match 2.9%; Score 21; DB 3; Length 5156;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 475 GAAATTAATTAATTAATTT 495
 DB 537 GAAATTAATTAATTAATTT 557

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: October 15, 2004, 00:15:17
Job time : 517.316 secs

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OM nucleic - nucleic search, using sm model

Run on: October 14, 2004, 22:42:59 ; Search time 3337.09 Seconds

(without alignments)
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SUMMARIES

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29: gb_gss2:*
Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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c 166	20	2.8	1052	28	CC299800	CC299800	223	19	2.7	366	12	B1142805	B1142805	FK74c03.y
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172	19	2.7	117	13	BO504400	BO504400	229	19	2.7	374	9	AA703589	AA703589	214e10.s
173	19	2.7	159	13	C93393	C93393	230	19	2.7	375	9	AA647881	AA647881	ed10e12.s
c 174	19	2.7	163	12	BP520062	BP520062	231	19	2.7	375	28	CC448752	CC448752	ZMM8BC033
175	19	2.7	171	12	BP110639	BP110639	232	19	2.7	379	12	BG731836	BG731836	PS08f03.y
176	19	2.7	196	9	AV379414	AV379414	233	19	2.7	380	12	BW881940	BW881940	FK54a03.y
177	19	2.7	203	29	BK202617	BK202617	234	19	2.7	385	13	BQ371932	BQ371932	CM1-FN004
c 178	19	2.7	208	10	BB351170	BB351170	235	19	2.7	386	12	BG736193	BG736193	FK52h12.y
c 179	19	2.7	208	29	AL766117	AL766117	236	19	2.7	386	14	D32818	D32818	CELK021H9R
c 180	19	2.7	225	29	CR482419	CR482419	237	19	2.7	394	28	AQ684349	AQ684349	HS_5493.B
c 181	19	2.7	228	10	AW727519	AW727519	238	19	2.7	395	12	BJ117668	BJ117668	AL749365
c 182	19	2.7	229	10	AW468425	AW468425	239	19	2.7	395	29	DR5M6T	DR5M6T	AL653697
c 183	19	2.7	230	12	BP520251	BP520251	240	19	2.7	397	10	BF056222	BF056222	7K74c03.x
c 184	19	2.7	234	10	BB334288	BB334288	241	19	2.7	397	12	BF736153	BF736153	FK52a02.y
185	19	2.7	237	10	BB078492	BB078492	242	19	2.7	401	14	CK233615	CK233615	FK69g06.y
c 186	19	2.7	239	9	AA218960	AA218960	243	19	2.7	402	12	BG736087	BG736087	FK69g12.y
c 187	19	2.7	239	10	BB095758	BB095758	244	19	2.7	402	12	CK233615	CK233615	FK69g12.y
188	19	2.7	240	9	AU074851	AU074851	245	19	2.7	410	9	AA831233	AA831233	0c66f11.s
189	19	2.7	240	13	BW005725	BW005725	246	19	2.7	411	14	CB178336	CB178336	0c66f11.s
190	19	2.7	243	10	BB076700	BB076700	247	19	2.7	413	13	BK554592	BK554592	FK52g07.y
c 191	19	2.7	249	9	AI668215	AI668215	248	19	2.7	414	14	CK233362	CK233362	FK52g07.y
c 192	19	2.7	265	9	AL880542	AL880542	249	19	2.7	415	28	AQ178997	AQ178997	HS_3071.B
c 193	19	2.7	265	10	BB178019	BB178019	250	19	2.7	417	13	BQ519962	BQ519962	NISG_n102
c 194	19	2.7	268	10	BF416195	BF416195	251	19	2.7	418	10	BG045154	BG045154	sa83Bc12-
c 195	19	2.7	278	9	AL852309	AL852309	252	19	2.7	418	13	BQ394801	BQ394801	NISG_n911
c 196	19	2.7	289	9	AA360820	AA360820	253	19	2.7	418	14	W23559	W23559	za45f08.f1
197	19	2.7	284	29	CG979141	CG979141	254	19	2.7	424	14	NA6018	NA6018	yy35d03.f1
c 198	19	2.7	300	9	AV200618	AV200618	255	19	2.7	426	13	BY218003	BY218003	BY218003
199	19	2.7	300	12	BM161949	BM161949	256	19	2.7	428	29	CE443821	CE443821	tl6f-gss-
200	19	2.7	300	13	C35274	C35274	257	19	2.7	432	10	BF367589	BF367589	tl6f-gss-
201	19	2.7	300	13	C35215	C35215	258	19	2.7	432	13	BY690431	BY690431	tl6f-gss-
202	19	2.7	300	13	C35124	C35124	259	19	2.7	435	13	BY696925	BY696925	tl6f-gss-
203	19	2.7	310	12	BI441504	BI441504	260	19	2.7	436	12	BG507832	BG507832	sa82Bc09.
c 204	19	2.7	320	10	BB132470	BB132470	261	19	2.7	441	14	N69666	N69666	za26d06.s1
c 205	19	2.7	325	9	AV216258	AV216258	262	19	2.7	442	28	AQ214088	AQ214088	HS_2187.B
c 206	19	2.7	325	10	BB520928	BB520928	263	19	2.7	446	9	AA457598	AA457598	aa80a10.f
208	19	2.7	325	14	D64416	D64416	264	19	2.7	448	29	CE647591	CE647591	tl6f-gss-
209	19	2.7	328	10	BB204271	BB204271	265	19	2.7	448	12	AM629817	AM629817	hnl1c07.y
210	19	2.7	328	10	BB057293	BB057293	266	19	2.7	448	12	BU032477	BU032477	BU032477
c 211	19	2.7	333	29	CA895421	CA895421	267	19	2.7	450	14	HS2303	HS2303	yy81d03.f1
c 212	19	2.7	334	14	CA895525	CA895525	268	19	2.7	450	28	AQ700914	AQ700914	HS_2116.A
213	19	2.7	338	29	CE718067	CE718067	269	19	2.7	454	10	BF428484	BF428484	ed10d01.
214	19	2.7	341	12	BI744787	BI744787	270	19	2.7	455	12	BM163004	BM163004	ed10d01.
215	19	2.7	344	12	BB735597	BB735597	271	19	2.7	455	29	CC472367	CC472367	ed10d01.
c 216	19	2.7	346	14	CD665546	CD665546	272	19	2.7	456	14	CB740432	CB740432	AM6ND0CM
							273	19	2.7	457	14	CF252523	CF252523	hdmn12B_c

274	19	2.7	462	28	AZ420625	AZ420625	1M0198J04	c 331	19	2.7	544	13	BQ526363	BQ526363	NISC.no15
275	19	2.7	464	10	AM654060	AM654060	103289 NA	332	19	2.7	544	28	AZ437376	AZ437376	1M0228B07
276	19	2.7	466	14	CA896529	CA896529	B0199601-	333	19	2.7	544	28	BH266293	BH266293	CH230-19A
277	19	2.7	468	14	CB094415	CB094415	hz69903.b	c 334	19	2.7	544	29	CE228921	CE228921	tiqr-gss-
278	19	2.7	469	12	BI323699	BI323699	kt66d02.y	c 335	19	2.7	547	29	TA229H06P	TA229H06P	tiqr-gss-
279	19	2.7	469	14	CB340513	CB340513	CA23E1021	c 336	19	2.7	548	28	AQ668971	AQ668971	T. brucei
280	19	2.7	470	12	BI941803	BI941803	ed16h11.y	c 337	19	2.7	550	9	A1867689	A1867689	HS_3432_A
281	19	2.7	471	28	AQ402206	AQ402206	HS_5061_A	c 338	19	2.7	552	13	BK692261	BK692261	bx692261
282	19	2.7	476	29	CE114633	CE114633	tiqr-gss-	c 339	19	2.7	554	28	B2520134	B2520134	BQKQ5277F
283	19	2.7	476	29	CE114633	CE114633	tiqr-gss-	c 340	19	2.7	555	10	BE551202	BE551202	7b55r11.x
284	19	2.7	477	9	AU284006	AU284006	AU284006	341	19	2.7	555	12	BM340125	BM340125	MEF318-C
285	19	2.7	478	12	BM689555	BM689555	UI-E-CK1-	342	19	2.7	556	14	CF611163	CF611163	LEF-C22CF-
286	19	2.7	479	13	BO837507	BO837507	rE27-c03.y	c 343	19	2.7	557	14	CF342383	CF342383	PLNc1-70
287	19	2.7	480	14	D27726	D27726	CELK003A1R	c 344	19	2.7	558	13	BU495660	BU495660	Pfnc1-70
288	19	2.7	483	28	AQ134812	AQ134812	HS_3053_A	c 345	19	2.7	560	28	AZ398909	AZ398909	BU495660 Pfnc1-70
289	19	2.7	484	14	CA820036	CA820036	saub3f04.	c 346	19	2.7	563	12	BI105752	BI105752	AZ398909 B0164G01
290	19	2.7	485	13	BQ391614	BQ391614	NISC.mq19	c 347	19	2.7	563	12	BM431782	BM431782	B0164G01 B02892350
291	19	2.7	485	14	CD420243	CD420243	r184b01.y	c 348	19	2.7	564	14	CB441727	CB441727	fm62d05.y
292	19	2.7	487	14	CB340092	CB340092	CA23E1021	349	19	2.7	564	28	BH063420	BH063420	fm62d05.y
293	19	2.7	489	9	A1477816	A1477816	td55d08.y	c 350	19	2.7	564	29	BX231608	BX231608	RPc1-24-2
294	19	2.7	490	29	DN13M2S	DN13M2S	Dnlo ref	c 351	19	2.7	565	14	CB442066	CB442066	RPc1-24-2
295	19	2.7	491	29	AG237448	AG237448	Lotus cor	352	19	2.7	566	12	BP112817	BP112817	Lotus cor
296	19	2.7	494	9	AA238317	AA238317	mx28c03.r	353	19	2.7	567	10	AW274139	AW274139	xv27-c07.x
297	19	2.7	494	29	CE259868	CE259868	tiqr-gss-	354	19	2.7	568	12	BG620355	BG620355	602618664
298	19	2.7	494	29	CE494949	CE494949	tiqr-gss-	355	19	2.7	569	13	BQ837147	BQ837147	602618664
299	19	2.7	497	14	CB538086	CB538086	776047 NA	c 356	19	2.7	570	14	CA679810	CA679810	w1m4.pK00
300	19	2.7	499	10	AM851044	AM851044	IL3-C7022	c 357	19	2.7	571	12	BM271827	BM271827	1g35f05.y
301	19	2.7	499	10	AM942134	AM942134	LD10457.3	c 358	19	2.7	573	12	BM424963	BM424963	1g35f05.y
302	19	2.7	500	13	BU786488	BU786488	ln55e01.y	c 359	19	2.7	574	13	BQ519987	BQ519987	MEET25-H
303	19	2.7	500	29	CC792499	CC792499	ZMMBBP016	c 360	19	2.7	574	28	AQ122465	AQ122465	NISC.p102
304	19	2.7	502	29	CE773414	CE773414	tiqr-gss-	c 361	19	2.7	577	29	CE616770	CE616770	HS_3080_A
305	19	2.7	504	28	AQ171244	AQ171244	HS_073.B	c 362	19	2.7	578	28	AZ015412	AZ015412	tiqr-gss-
306	19	2.7	505	13	BY654475	BY654475	BS654475	c 363	19	2.7	578	28	AQ563332	AQ563332	RPc1-23-3
307	19	2.7	506	14	CB500570	CB500570	saalga503	c 364	19	2.7	579	10	BF025321	BF025321	dg01f05.x
308	19	2.7	509	12	BG882533	BG882533	saalmd50	c 365	19	2.7	580	29	CE632886	CE632886	tiqr-gss-
309	19	2.7	511	28	AQ470602	AQ470602	CITB1-E1-	c 366	19	2.7	584	29	DR24C2S	DR24C2S	tiqr-gss-
310	19	2.7	511	28	AQ470602	AQ470602	CITB1-E1-	c 367	19	2.7	588	12	BI773483	BI773483	Dnlo ref
311	19	2.7	513	13	BU660295	BU660295	Dnlo ref	c 368	19	2.7	589	13	BU277083	BU277083	r467c06.y
312	19	2.7	513	13	BU660295	BU660295	ci158d08.2	c 369	19	2.7	591	14	CB424361	CB424361	598607 NA
313	19	2.7	513	28	AZ806362	AZ806362	2M0068B23	c 370	19	2.7	591	28	AQ658225	AQ658225	Sheared D
314	19	2.7	519	29	CE735152	CE735152	tiqr-gss-	c 371	19	2.7	591	29	CE281617	CE281617	tiqr-gss-
315	19	2.7	523	13	CA042041	CA042041	saalplnd5	c 372	19	2.7	595	28	BH616717	BH616717	tiqr-gss-
316	19	2.7	524	13	BQ548554	BQ548554	rd33a07.y	c 373	19	2.7	596	9	AV864501	AV864501	AV864501
317	19	2.7	524	14	CA455691	CA455691	AGBNOCURT	c 374	19	2.7	596	13	BQ534426	BQ534426	H4028A11-
318	19	2.7	526	28	BZ543445	BZ543445	OGA.X13TM	c 375	19	2.7	597	9	AV894275	AV894275	H4028A11-
319	19	2.7	526	29	CE546095	CE546095	tiqr-gss-	c 376	19	2.7	597	28	B2302361	B2302361	AV894275
320	19	2.7	527	29	AG240771	AG240771	Lotus cor	c 377	19	2.7	598	29	CE446377	CE446377	tiqr-gss-
321	19	2.7	528	9	AM060874	AM060874	UI-M-BH1-	378	19	2.7	599	28	BZ294691	BZ294691	CG1046.r1
322	19	2.7	529	29	TA103E08P	TA103E08P	UI-M-BH1-	379	19	2.7	600	14	CA302194	CA302194	CG1046.r1
323	19	2.7	530	29	TA2E10Q	TA2E10Q	T. brucei	380	19	2.7	601	12	BP514191	BP514191	CG1046.r1
324	19	2.7	533	10	BF223590	BF223590	uy43605.x	381	19	2.7	602	28	AQ563263	AQ563263	HS_5334.B
325	19	2.7	533	28	BH665528	BH665528	BOMWCB3TF	382	19	2.7	603	29	CE776298	CE776298	tiqr-gss-
326	19	2.7	535	10	BG006047	BG006047	PM2-GH001	c 383	19	2.7	604	28	BH782530	BH782530	fm62d05.y
327	19	2.7	535	12	BM166586	BM166586	EST569109	c 384	19	2.7	606	13	BQ393720	BQ393720	NISC.ng05
328	19	2.7	536	14	CP562341	CP562341	B0446010-	c 385	19	2.7	610	29	CE304344	CE304344	tiqr-gss-
329	19	2.7	538	12	BJ089342	BJ089342	B089342	c 386	19	2.7	611	28	AZ314835	AZ314835	tiqr-gss-
330	19	2.7	541	28	AQ202671	AQ202671	RPc111-58	387	19	2.7	612	12	BJ359400	BJ359400	tiqr-gss-

388	19	2.7	617	14	CB350642	CS350642	ME57233-H	c 445	19	2.7	689	28	CC079287	CC079287	CSU-K33r.
c 389	19	2.7	617	28	AQ736017	AQ736017	HS_303_B	c 446	19	2.7	689	29	BX124857	BX124857	re
390	19	2.7	619	12	BM349128	BM349128	ME57308-G	447	19	2.7	691	29	CE476214	CE476214	tiqr-gsa-
c 391	19	2.7	619	28	AQ440977	AQ440977	HS_5109_A	c 448	19	2.7	696	14	CD232746	CD232746	FNPA904
c 392	19	2.7	620	29	DR1B55	DR1B55	AL732851	449	19	2.7	697	14	CB550058	CB550058	MFL0001-
393	19	2.7	621	29	CE422296	CE422296	tiqr-gsa-	c 450	19	2.7	697	29	CE425276	CE425276	tiqr-gsa-
c 394	19	2.7	622	14	CA941124	CA941124	tiqr-gsa-	c 451	19	2.7	699	29	CC729516	CC729516	OGJWB17H
395	19	2.7	622	13	BU548346	BU548346	GM890015A	c 452	19	2.7	700	28	BH999538	BH999538	oe996h08.
396	19	2.7	629	13	BM282172	BM282172	BM282172	c 453	19	2.7	702	29	CE150919	CE150919	tiqr-gsa-
c 397	19	2.7	631	9	AI991575	AI991575	wa17h07.x	c 454	19	2.7	705	13	BM005593	BM005593	tiqr-gsa-
398	19	2.7	632	28	AZ665806	AZ665806	1M0547M19	c 455	19	2.7	706	13	BU278424	BU278424	603862766
c 399	19	2.7	634	29	CE256127	CE256127	tiqr-gsa-	c 456	19	2.7	706	29	CE630215	CE630215	tiqr-gsa-
c 400	19	2.7	635	9	AU220273	AU220273	AU220273	c 457	19	2.7	707	13	BY751241	BY751241	tiqr-gsa-
c 401	19	2.7	635	10	BF055342	BF055342	7K60f04.x	c 458	19	2.7	707	28	AZ937008	AZ937008	2M0195106
c 402	19	2.7	636	14	CS0506048	CS0506048	ssalmgd50	c 459	19	2.7	708	13	BM034467	BM034467	BM034467
403	19	2.7	637	10	BF294221	BF294221	001PbF04	c 460	19	2.7	708	28	AQ266709	AQ266709	BM034467
404	19	2.7	637	10	BF299668	BF299668	026PbC09	c 461	19	2.7	714	12	BP178228	BP178228	BM034467
405	19	2.7	638	29	DR49C15T	DR49C15T	Danlo rer	c 462	19	2.7	715	28	BZ602244	BZ602244	tiqr-gsa-
406	19	2.7	639	28	AQ485713	AQ485713	RPCI-11-2	c 463	19	2.7	716	29	CE775183	CE775183	tiqr-gsa-
c 407	19	2.7	640	13	BO628557	BO628557	rd17b12.y	c 464	19	2.7	718	10	BF270796	BF270796	GA_EB000
c 408	19	2.7	642	29	CE734819	CE734819	tiqr-gsa-	c 465	19	2.7	718	28	AZ986420	AZ986420	tiqr-gsa-
c 409	19	2.7	645	12	BJ346819	BJ346819	tiqr-gsa-	c 466	19	2.7	721	28	AZ945675	AZ945675	tiqr-gsa-
c 410	19	2.7	645	29	CB144106	CB144106	tiqr-gsa-	c 467	19	2.7	724	29	CE726051	CE726051	tiqr-gsa-
c 411	19	2.7	646	10	BB629495	BB629495	BB629495	c 468	19	2.7	725	28	CC439369	CC439369	PURP142TB
c 412	19	2.7	646	13	BM107597	BM107597	BM107597	c 469	19	2.7	726	29	BM243038	BM243038	Danlo rer
c 413	19	2.7	647	29	CB838433	CB838433	tiqr-gsa-	c 470	19	2.7	727	13	BM164058	BM164058	tiqr-gsa-
c 414	19	2.7	648	13	BM108762	BM108762	BM108762	c 471	19	2.7	736	29	AG000634	AG000634	tiqr-gsa-
c 415	19	2.7	649	9	AL853656	AL853656	AL853656	c 472	19	2.7	740	13	BU333334	BU333334	tiqr-gsa-
416	19	2.7	649	9	AV975733	AV975733	AV975733	c 473	19	2.7	740	29	BX150410	BX150410	tiqr-gsa-
417	19	2.7	649	13	BM295505	BM295505	BM295505	c 474	19	2.7	741	29	CE353251	CE353251	Danlo rer
418	19	2.7	651	9	AV700676	AV700676	AV700676	c 475	19	2.7	744	14	CD100787	CD100787	tiqr-gsa-
419	19	2.7	651	28	AZ521527	AZ521527	RPCI-11-1	c 476	19	2.7	750	29	BX221241	BX221241	tiqr-gsa-
c 420	19	2.7	653	29	AG117369	AG117369	Pan trogl	c 477	19	2.7	756	29	CG989326	CG989326	tiqr-gsa-
c 421	19	2.7	657	28	BH004778	BH004778	BMAC08J1	c 478	19	2.7	757	13	BY769681	BY769681	tiqr-gsa-
422	19	2.7	660	29	CE149202	CE149202	tiqr-gsa-	c 479	19	2.7	758	14	CD104631	CD104631	tiqr-gsa-
c 423	19	2.7	661	29	CE782973	CE782973	tiqr-gsa-	c 480	19	2.7	758	14	CD454571	CD454571	tiqr-gsa-
c 424	19	2.7	662	12	BP020628	BP020628	tiqr-gsa-	c 481	19	2.7	760	14	CA772412	CA772412	tiqr-gsa-
c 425	19	2.7	662	13	BY723108	BY723108	tiqr-gsa-	c 482	19	2.7	761	29	CG230325	CG230325	tiqr-gsa-
c 426	19	2.7	662	28	BH003097	BH003097	BMAC03P1	c 483	19	2.7	761	29	CE272943	CE272943	tiqr-gsa-
c 427	19	2.7	663	13	BU332377	BU332377	603870712	c 484	19	2.7	764	29	CC337156	CC337156	tiqr-gsa-
c 428	19	2.7	664	9	AL881289	AL881289	AL881289	c 485	19	2.7	769	28	CC337156	CC337156	tiqr-gsa-
429	19	2.7	664	12	BP025084	BP025084	BP025084	c 486	19	2.7	771	14	CB148193	CB148193	tiqr-gsa-
430	19	2.7	666	28	AZ947047	AZ947047	2M0209C12	c 487	19	2.7	771	14	CB958319	CB958319	tiqr-gsa-
431	19	2.7	666	29	AG177682	AG177682	Pan trogl	c 488	19	2.7	772	28	BZ392380	BZ392380	tiqr-gsa-
432	19	2.7	668	14	CB889620	CB889620	tae39e04.	c 489	19	2.7	772	29	EX174232	EX174232	tiqr-gsa-
c 433	19	2.7	668	29	CE621964	CE621964	tiqr-gsa-	c 490	19	2.7	773	29	CG956685	CG956685	tiqr-gsa-
c 434	19	2.7	670	9	AI652883	AI652883	tiqr-gsa-	c 491	19	2.7	774	14	CD854177	CD854177	tiqr-gsa-
c 435	19	2.7	673	28	BZ044209	BZ044209	tiqr-gsa-	c 492	19	2.7	774	14	CD889997	CD889997	tiqr-gsa-
c 436	19	2.7	675	28	CE066013	CE066013	MUGO CH25	c 493	19	2.7	775	29	QNS0612C	QNS0612C	tiqr-gsa-
437	19	2.7	679	12	BM170134	BM170134	ESF57657	c 494	19	2.7	776	14	CB316981	CB316981	tiqr-gsa-
438	19	2.7	679	28	BH115952	BH115952	RPCI11-56	c 495	19	2.7	776	14	BZ228418	BZ228418	tiqr-gsa-
439	19	2.7	680	28	BZ021013	BZ021013	oe170F07.	c 496	19	2.7	777	14	CK095796	CK095796	tiqr-gsa-
440	19	2.7	680	29	CG026885	CG026885	PGAA10TF	c 497	19	2.7	778	28	CC313785	CC313785	tiqr-gsa-
441	19	2.7	682	12	BZ044940	BZ044940	tiqr-gsa-	c 498	19	2.7	781	29	CG934012	CG934012	tiqr-gsa-
442	19	2.7	682	13	BX103776	BX103776	tiqr-gsa-	c 499	19	2.7	783	29	EX195877	EX195877	tiqr-gsa-
c 443	19	2.7	684	28	BH71973	BH71973	tiqr-gsa-	c 500	19	2.7	783	29	BX208600	BX208600	tiqr-gsa-
c 444	19	2.7	684	29	CB836784	CB836784	tiqr-gsa-	c 501	19	2.7	785	28	AZ183662	AZ183662	tiqr-gsa-

c 502	19	2.7	788	29	AG117202	Pen troc1	c 559	19	2.7	893	28	BH162930
503	19	2.7	793	13	BX712643	BX712643	560	19	2.7	894	28	B2189413
504	19	2.7	793	28	B2967958	B2967958	561	19	2.7	895	10	BF701802
505	19	2.7	796	28	BH452975	BH452975	562	19	2.7	897	28	A2541767
c 506	19	2.7	797	28	BH280987	BH280987	563	19	2.7	898	10	BF781504
507	19	2.7	801	29	CL003464	ghst1 YMS	c 564	19	2.7	898	28	A2536300
c 508	19	2.7	804	29	CC539978	CH240_420	c 565	19	2.7	899	28	A2535398
509	19	2.7	805	29	CNS07C/N	AI439689 T3 end of	c 566	19	2.7	900	13	BX347911
c 510	19	2.7	807	29	CC283053	OGMA19TH	567	19	2.7	900	13	BX347911
511	19	2.7	809	28	B2172373	B2172373	c 568	19	2.7	902	13	BX327950
512	19	2.7	809	29	CC637088	OGJF142TV	c 569	19	2.7	902	13	BX327950
513	19	2.7	812	14	CD248121	CC248121	570	19	2.7	903	28	BH146542
514	19	2.7	817	28	BH682324	BH682324	c 571	19	2.7	904	28	BH146542
c 515	19	2.7	824	13	BU234266	BU234266	c 572	19	2.7	904	28	A2548896
516	19	2.7	825	14	CF783233	CF783233	573	19	2.7	904	28	BH158848
517	19	2.7	825	29	CC960768	CC960768	574	19	2.7	904	29	CC543155
518	19	2.7	825	29	CNS02VTV	AL215428 Tetradon	c 575	19	2.7	905	28	A2680096
c 519	19	2.7	826	29	CC497738	CC497738	c 576	19	2.7	905	28	A2680096
c 520	19	2.7	830	29	CC242409	CC242409	c 577	19	2.7	905	28	A2680096
c 521	19	2.7	833	12	BG614457	BG614457	578	19	2.7	905	28	BH161020
522	19	2.7	833	13	BUS99915	BUS99915	579	19	2.7	910	28	A2534544
c 523	19	2.7	835	29	CC308499	CC308499	c 580	19	2.7	911	29	CC947182
c 524	19	2.7	836	28	B2967960	B2967960	c 581	19	2.7	912	29	CC850900
c 525	19	2.7	837	28	A2545464	A2545464	582	19	2.7	915	29	CC858256
c 526	19	2.7	841	28	B2389758	B2389758	583	19	2.7	919	28	BH155121
527	19	2.7	843	28	BH329541	BH329541	584	19	2.7	919	29	CC262858
528	19	2.7	844	13	BUS61414	BUS61414	c 585	19	2.7	922	29	CC058255
c 529	19	2.7	844	29	BK197708	BK197708	c 586	19	2.7	924	28	B2461056
c 530	19	2.7	846	10	BF099935	BF099935	587	19	2.7	928	28	BH131549
c 531	19	2.7	847	28	B2172013	B2172013	588	19	2.7	929	29	CC948428
c 532	19	2.7	849	14	CP653176	CP653176	589	19	2.7	934	28	B2817964
533	19	2.7	849	28	B2223908	B2223908	c 590	19	2.7	941	28	B2401222
c 534	19	2.7	851	28	BH478351	BH478351	591	19	2.7	941	29	CC261453
535	19	2.7	852	28	AQ747606	AQ747606	c 592	19	2.7	945	29	CNS01054
536	19	2.7	852	28	A2210572	A2210572	c 593	19	2.7	947	28	BH134574
537	19	2.7	853	28	A2681952	A2681952	594	19	2.7	949	28	B2817968
538	19	2.7	854	28	B2395298	B2395298	595	19	2.7	956	10	BF783073
539	19	2.7	856	28	A2684744	A2684744	c 596	19	2.7	967	28	CC283065
c 540	19	2.7	857	28	BH138970	BH138970	597	19	2.7	967	28	AQ749130
541	19	2.7	858	28	A2190348	A2190348	c 598	19	2.7	986	12	B1868921
c 542	19	2.7	860	13	BK699033	BK699033	c 599	19	2.7	988	28	CC274721
c 543	19	2.7	864	12	BG615614	BG615614	c 600	19	2.7	992	29	CNS060CT
544	19	2.7	864	12	BG741231	BG741231	c 601	19	2.7	1006	28	CC190264
c 545	19	2.7	866	13	BUS60984	BUS60984	602	19	2.7	1014	28	A2935655
c 546	19	2.7	867	29	CC698239	CC698239	603	19	2.7	1035	28	CC213932
547	19	2.7	867	29	CC946868	CC946868	604	19	2.7	1041	29	CNS06025
c 548	19	2.7	868	28	BH162606	BH162606	605	19	2.7	1045	28	CC209722
c 549	19	2.7	870	28	B2155101	B2155101	606	19	2.7	1087	12	BG494028
c 550	19	2.7	871	29	CC262867	CC262867	607	19	2.7	1090	29	CC432105
c 551	19	2.7	872	29	CC9556113	CC9556113	608	19	2.7	1101	29	CNS0021X
552	19	2.7	873	29	CG141255	CG141255	609	19	2.7	1101	29	CNS0021X
c 553	19	2.7	876	14	CF548426	CF548426	610	19	2.7	1101	29	CNS0031F
c 554	19	2.7	878	14	CF935846	CF935846	611	19	2.7	1109	28	CC275353
555	19	2.7	886	10	BF682967	BF682967	c 612	19	2.7	1127	28	CC281206
c 556	19	2.7	888	28	BH154884	BH154884	c 613	19	2.7	1151	13	BUS08171
557	19	2.7	889	28	B2089038	B2089038	614	19	2.7	1156	28	CC303531
c 558	19	2.7	890	13	BUS09912	BUS09912	615	19	2.7	1164	14	CC209747

616	19	2.7	1201	AL560964	AL560964	672	18	2.5	183	14	CF381807	CF381807	1ab84c07.	
617	19	2.7	1201	9	AL563531	673	18	2.5	184	14	CF426422	CF426422	1ad24b12.	
618	19	2.7	1219	10	BE781637	674	18	2.5	185	14	CF383391	CF383391	1ac64f06.	
619	19	2.7	1404	28	EK557894	675	18	2.5	186	12	BM055280	BM055280	1ae92b03.-y-	
620	19	2.7	1344	29	AV413870	676	18	2.5	186	29	CE207306	CE207306	ti9r-g9s-	
621	19	2.7	1650	29	AV413868	677	18	2.5	187	13	BM743121	BM743121	UI-E-BJ1-	
622	19	2.7	4663	11	BC030769	678	18	2.5	187	14	CF382821	CF382821	1ac68e10.	
623	18	2.5	40	28	BM789828	679	18	2.5	188	9	AI376105	AI376105	ta0d4d03.x	
624	18	2.5	43	9	AM059808	680	18	2.5	191	14	CF424659	CF424659	1ad35a11.	
625	18	2.5	46	14	ID5636	681	18	2.5	191	14	CF9227071	CF9227071	1af46b09.	
626	18	2.5	72	28	BE763918	682	18	2.5	194	14	CB446279	CB446279	9688081.NM	
627	18	2.5	111	9	AA421204	683	18	2.5	194	14	CF353798	CF353798	1ab86801.	
628	18	2.5	113	9	AU009118	684	18	2.5	194	29	CS511245	CS511245	OSM53505	
c 629	18	2.5	121	9	AI352692	685	18	2.5	195	10	BM324211	BM324211	BSK62311	
	18	2.5	125	9	AA323680	686	18	2.5	195	12	B1647150	B1647150	6032799606	
	18	2.5	126	9	AU284784	687	18	2.5	195	13	BY662126	BY662126	BY662126	
	18	2.5	139	9	AI810691	688	18	2.5	195	14	CB445920	CB445920	697308.NM	
	18	2.5	142	28	BH168951	689	18	2.5	195	14	CF379492	CF379492	1ac687c06.	
	18	2.5	149	9	AU269464	690	18	2.5	197	9	AI340977	AI340977	9682f02.-x	
	18	2.5	149	10	BM067692	691	18	2.5	197	9	AV467121	AV467121	AV367121	
	18	2.5	152	13	BE434109	692	18	2.5	197	9	AV457888	AV457888	AV347968	
	18	2.5	154	10	BM434146	693	18	2.5	197	14	CB893802	CB893802	ES764659	
	18	2.5	154	10	BH050827	694	18	2.5	198	10	BM424668	BM424668	BM424668	
637	18	2.5	154	13	BM050827	695	18	2.5	198	28	BH296887	BH296887	CH230-140f	
638	18	2.5	154	14	CF423792	696	18	2.5	199	10	BM117652	BM117652	BM117652	
639	18	2.5	154	14	CF423792	697	18	2.5	199	10	BM429019	BM429019	BM429019	
640	18	2.5	155	10	BM056958	698	18	2.5	199	10	BM510631	BM510631	BM510631	
641	18	2.5	156	9	AV338254	699	18	2.5	199	10	BM510631	BM510631	BM510631	
642	18	2.5	157	9	AV173236	700	18	2.5	199	10	BE926443	BE926443	UI-W-B21-	
643	18	2.5	157	29	CC718274	701	18	2.5	199	12	BM792733	BM792733	BM792733	
644	18	2.5	159	10	BM535931	702	18	2.5	200	9	AV233498	AV233498	AV233498	
645	18	2.5	159	10	BE788415	703	18	2.5	200	10	BM427162	BM427162	BM427162	
646	18	2.5	159	14	CD537088	704	18	2.5	200	10	BM430543	BM430543	BM430543	
647	18	2.5	160	9	AA768714	705	18	2.5	200	10	BM453893	BM453893	BM453893	
648	18	2.5	160	10	AV326756	706	18	2.5	200	10	BM729357	BM729357	BM729357	
649	18	2.5	161	29	CF763829	707	18	2.5	200	14	CB645165	CB645165	1ab20a08.	
650	18	2.5	162	14	CF621859	708	18	2.5	200	14	CB645383	CB645383	1ab21c09.	
651	18	2.5	163	14	CF239840	709	18	2.5	201	10	BM049797	BM049797	BM049797	
652	18	2.5	163	10	BM062122	710	18	2.5	201	10	BM098457	BM098457	BM098457	
653	18	2.5	165	165	28	A2720377	711	18	2.5	201	10	BM274466	BM274466	BM274466
654	18	2.5	166	14	CF382320	712	18	2.5	201	14	CA337195	CA337195	NISC-1V10C	
655	18	2.5	167	14	CF382669	713	18	2.5	202	9	AV330922	AV330922	AV330922	
656	18	2.5	169	9	AV247469	714	18	2.5	202	10	BM428196	BM428196	BM428196	
657	18	2.5	170	9	AV150999	715	18	2.5	202	29	CE028931	CE028931	ti9r-g9s-	
658	18	2.5	170	3	BM947176	716	18	2.5	203	9	AI450819	AI450819	me88e03.x	
659	18	2.5	172	14	CB105024	717	18	2.5	203	9	AI450684	AI450684	AV336084	
660	18	2.5	172	14	CF423578	718	18	2.5	203	10	BM305072	BM305072	BM305072	
661	18	2.5	172	14	CF423349	719	18	2.5	203	10	BM057089	BM057089	BM057089	
662	18	2.5	173	9	AV314003	720	18	2.5	203	10	BM059233	BM059233	BM059233	
663	18	2.5	173	14	CF926285	721	18	2.5	203	10	BM057990	BM057990	BM057990	
664	18	2.5	174	14	CF804353	722	18	2.5	203	10	BM059233	BM059233	BM059233	
665	18	2.5	174	14	CF804722	723	18	2.5	203	10	BM306194	BM306194	BM306194	
666	18	2.5	177	14	CF381830	724	18	2.5	203	10	BM343698	BM343698	BM343698	
667	18	2.5	179	14	CF353594	725	18	2.5	203	10	BM414998	BM414998	BM414998	
668	18	2.5	180	28	B48430	726	18	2.5	204	10	BM150848	BM150848	BM150848	
669	18	2.5	182	29	CE654869	727	18	2.5	205	9	AV340717	AV340717	AV340717	
670	18	2.5	183	9	AV381989	728	18	2.5	205	9	AV379331	AV379331	AV379331	
671	18	2.5	183	12	BM930437	729	18	2.5	205	10	BM022579	BM022579	BM022579	

729	c	730	18	2.5	205	10	BB38B073	BB38B073	BB38B073	c	786	18	2.5	249	9	AV366712	AV366712	AV366712
730	c	731	18	2.5	205	29	CE050396	CE050396	CE050396	c	787	18	2.5	249	9	AV020412	AV020412	AV020412
731	c	732	18	2.5	205	29	CE803774	CE803774	CE803774	c	788	18	2.5	250	9	AV342057	AV342057	AV342057
732	c	733	18	2.5	206	10	BB049692	BB049692	BB049692	c	789	18	2.5	251	9	AV972335	AV972335	AV972335
733	c	734	18	2.5	206	10	BB049895	BB049895	BB049895	c	790	18	2.5	252	10	BF007935	BF007935	BF007935
734	c	735	18	2.5	206	10	BB074437	BB074437	BB074437	c	791	18	2.5	253	14	F04912	F04912	F04912
735	c	736	18	2.5	206	10	BB383079	BB383079	BB383079	c	792	18	2.5	254	13	BQ161436	BQ161436	BQ161436
736	c	737	18	2.5	206	10	BB431366	BB431366	BB431366	c	793	18	2.5	255	9	AV370086	AV370086	AV370086
737	c	738	18	2.5	206	14	CE894154	CE894154	CE894154	c	794	18	2.5	255	14	CF425741	CF425741	CF425741
738	c	739	18	2.5	207	10	BB389399	BB389399	BB389399	c	795	18	2.5	257	10	BB349946	BB349946	BB349946
739	c	740	18	2.5	208	10	BB422058	BB422058	BB422058	c	796	18	2.5	260	9	AV026126	AV026126	AV026126
740	c	741	18	2.5	209	10	BB545679	BB545679	BB545679	c	797	18	2.5	260	9	AV221882	AV221882	AV221882
741	c	742	18	2.5	211	10	AA066557	AA066557	AA066557	c	798	18	2.5	260	12	BQ440161	BQ440161	BQ440161
742	c	743	18	2.5	213	13	BB725399	BB725399	BB725399	c	799	18	2.5	261	9	AA874525	AA874525	AA874525
743	c	744	18	2.5	214	14	T29811	T29811	T29811	c	800	18	2.5	261	9	A1509496	A1509496	A1509496
744	c	745	18	2.5	214	28	AQ274991	AQ274991	AQ274991	c	801	18	2.5	263	12	B1493258	B1493258	B1493258
745	c	746	18	2.5	215	10	BF033650	BF033650	BF033650	c	802	18	2.5	265	9	AV330479	AV330479	AV330479
746	c	747	18	2.5	216	12	B1745308	B1745308	B1745308	c	803	18	2.5	265	9	AV334019	AV334019	AV334019
747	c	748	18	2.5	218	9	AV204192	AV204192	AV204192	c	804	18	2.5	265	9	AM089114	AM089114	AM089114
748	c	749	18	2.5	219	10	AM151417	AM151417	AM151417	c	805	18	2.5	265	14	W51650	W51650	W51650
749	c	750	18	2.5	221	13	BO567299	BO567299	BO567299	c	806	18	2.5	266	10	BB672376	BB672376	BB672376
750	c	751	18	2.5	222	14	N75587	N75587	N75587	c	807	18	2.5	266	10	BFI19344	BFI19344	BFI19344
751	c	752	18	2.5	223	9	AV369214	AV369214	AV369214	c	808	18	2.5	266	12	B1868626	B1868626	B1868626
752	c	753	18	2.5	224	14	CF614615	CF614615	CF614615	c	809	18	2.5	267	10	BB419364	BB419364	BB419364
753	c	754	18	2.5	228	9	AV365319	AV365319	AV365319	c	810	18	2.5	267	12	B1676747	B1676747	B1676747
754	c	755	18	2.5	229	9	AV355584	AV355584	AV355584	c	811	18	2.5	267	12	B1676780	B1676780	B1676780
755	c	756	18	2.5	231	9	A1639784	A1639784	A1639784	c	812	18	2.5	268	9	AV308652	AV308652	AV308652
756	c	757	18	2.5	232	9	AV323224	AV323224	AV323224	c	813	18	2.5	268	13	BX564024	BX564024	BX564024
757	c	758	18	2.5	232	10	BE113851	BE113851	BE113851	c	814	18	2.5	269	10	BB456740	BB456740	BB456740
758	c	759	18	2.5	233	9	A1550304	A1550304	A1550304	c	815	18	2.5	269	12	BM661731	BM661731	BM661731
759	c	760	18	2.5	234	29	CE691188	CE691188	CE691188	c	816	18	2.5	270	14	H31955	H31955	H31955
760	c	761	18	2.5	237	9	AV338744	AV338744	AV338744	c	817	18	2.5	271	9	AV330320	AV330320	AV330320
761	c	762	18	2.5	237	10	BB368359	BB368359	BB368359	c	818	18	2.5	272	12	BJ223534	BJ223534	BJ223534
762	c	763	18	2.5	237	10	BB538788	BB538788	BB538788	c	819	18	2.5	272	28	CC167590	CC167590	CC167590
763	c	764	18	2.5	237	10	BB541259	BB541259	BB541259	c	820	18	2.5	273	9	AV028985	AV028985	AV028985
764	c	765	18	2.5	239	14	CF355807	CF355807	CF355807	c	821	18	2.5	273	9	AV220414	AV220414	AV220414
765	c	766	18	2.5	239	14	CF425356	CF425356	CF425356	c	822	18	2.5	274	9	AV265537	AV265537	AV265537
766	c	767	18	2.5	240	12	B1054051	B1054051	B1054051	c	823	18	2.5	274	10	BB382706	BB382706	BB382706
767	c	768	18	2.5	240	14	CF754749	CF754749	CF754749	c	824	18	2.5	274	10	BB768360	BB768360	BB768360
768	c	769	18	2.5	240	28	B2580946	B2580946	B2580946	c	825	18	2.5	274	12	BM438991	BM438991	BM438991
769	c	770	18	2.5	240	29	CG787798	CG787798	CG787798	c	826	18	2.5	275	9	AA959879	AA959879	AA959879
770	c	771	18	2.5	242	10	AM206803	AM206803	AM206803	c	827	18	2.5	276	10	BB694958	BB694958	BB694958
771	c	772	18	2.5	243	9	AV349867	AV349867	AV349867	c	828	18	2.5	276	10	BB694958	BB694958	BB694958
772	c	773	18	2.5	243	9	AV371780	AV371780	AV371780	c	829	18	2.5	276	28	BH076100	BH076100	BH076100
773	c	774	18	2.5	243	10	AM324330	AM324330	AM324330	c	830	18	2.5	277	10	BB387115	BB387115	BB387115
774	c	775	18	2.5	243	28	BH033521	BH033521	BH033521	c	831	18	2.5	279	9	AV278240	AV278240	AV278240
775	c	776	18	2.5	244	14	CF388656	CF388656	CF388656	c	832	18	2.5	279	9	AV325490	AV325490	AV325490
776	c	777	18	2.5	245	9	AV233352	AV233352	AV233352	c	833	18	2.5	280	9	AV227278	AV227278	AV227278
777	c	778	18	2.5	245	9	AV372420	AV372420	AV372420	c	834	18	2.5	281	9	AV222042	AV222042	AV222042
778	c	779	18	2.5	246	9	AV353328	AV353328	AV353328	c	835	18	2.5	281	10	BB443305	BB443305	BB443305
779	c	780	18	2.5	246	10	BB855960	BB855960	BB855960	c	836	18	2.5	282	12	BM157933	BM157933	BM157933
780	c	781	18	2.5	246	12	BB993446	BB993446	BB993446	c	837	18	2.5	282	12	B1847639	B1847639	B1847639
781	c	782	18	2.5	246	28	B2387805	B2387805	B2387805	c	838	18	2.5	282	12	B1934450	B1934450	B1934450
782	c	783	18	2.5	247	9	AV282154	AV282154	AV282154	c	839	18	2.5	283	9	AA597632	AA597632	AA597632
783	c	784	18	2.5	247	28	B2356646	B2356646	B2356646	c	840	18	2.5	283	10	BB987778	BB987778	BB987778
784	c	785	18	2.5	247	28	B2356646	B2356646	B2356646	c	841	18	2.5	284	9	AV325600	AV325600	AV325600
785	c	786	18	2.5	247	28	B2356646	B2356646	B2356646	c	842	18	2.5	284	9	AV325600	AV325600	AV325600

c 843	18	2.5	284	10	AV438945	AV438945	x106d12.k	900	18	2.5	306	14	CA636303	CA636303	w1e1n.pk0
844	18	2.5	284	10	AW619812	AW619812	7880 MARC	901	18	2.5	307	12	B1079009	B1079009	602872270
845	18	2.5	284	12	B1079410	B1079410	602873806	902	18	2.5	307	14	H88302	H88302	y118f10.r1
c 846	18	2.5	284	14	W91688	W91688	M7A.F09..077	903	18	2.5	309	9	AT1805218	AT1805218	t14d46e12.x
847	18	2.5	285	10	BB074884	BB074884	BB074884	904	18	2.5	310	10	BB336524	BB336524	BB336524
848	18	2.5	285	10	BB383494	BB383494	BB383494	905	18	2.5	310	10	BB453350	BB453350	BB453350
c 849	18	2.5	285	10	BF222217	BF222217	7p44d01.k	906	18	2.5	311	9	AV104630	AV104630	AV104630
c 850	18	2.5	285	12	BS977377	BS977377	CM4-C1003	907	18	2.5	311	12	BG307784	BG307784	fms2910.y
c 851	18	2.5	286	14	F02262	F02262	HSCOUN102.n	908	18	2.5	312	9	AT1831607	AT1831607	w139f11.k
852	18	2.5	287	9	AV338359	AV338359	AV338359	909	18	2.5	312	9	AV220410	AV220410	AV220410
c 853	18	2.5	287	10	BB511457	BB511457	BB511457	910	18	2.5	313	9	AA287103	AA287103	z936f08.s
c 854	18	2.5	287	10	BB693629	BB693629	BB693629	911	18	2.5	313	28	BH644139	BH644139	BH644139
855	18	2.5	288	10	BB074833	BB074833	BB074833	912	18	2.5	314	9	AV220418	AV220418	AV220418
856	18	2.5	289	10	BB307613	BB307613	BB307613	913	18	2.5	314	12	BG994798	BG994798	PM0-HR091
857	18	2.5	290	10	BF451211	BF451211	uz66e07.k	914	18	2.5	314	13	BK266258	BK266258	BK266258
c 858	18	2.5	290	10	BB081909	BB081909	BB081909	915	18	2.5	314	13	BK275843	BK275843	BK275843
859	18	2.5	290	10	BB429405	BB429405	BB429405	916	18	2.5	314	14	CB053383	CB053383	N1C.G.9114
860	18	2.5	290	10	BB429557	BB429557	BB429557	917	18	2.5	315	10	BB547483	BB547483	BB547483
861	18	2.5	290	12	BM748950	BM748950	K-E370023	918	18	2.5	315	14	CK276031	CK276031	CK276031
c 862	18	2.5	290	14	H68303	H68303	y118f10..s1	919	18	2.5	315	14	CK276031	CK276031	ES7722109
c 863	18	2.5	291	9	AA917591	AA917591	o180f06.s	920	18	2.5	316	28	CC138332	CC138332	NDL.12G6.
864	18	2.5	291	9	AV119582	AV119582	AV119582	921	18	2.5	317	28	AO918893	AO918893	RPC1-23-2
865	18	2.5	291	9	AV338683	AV338683	AV338683	922	18	2.5	318	10	BB392958	BB392958	BB392958
c 866	18	2.5	291	10	BB119227	BB119227	BB119227	923	18	2.5	318	12	BO435241	BO435241	BO435241
c 867	18	2.5	291	10	BB181345	BB181345	BB181345	924	18	2.5	318	28	BH101972	BH101972	BE993025
c 868	18	2.5	293	10	BB130417	BB130417	BB130417	925	18	2.5	319	10	BE993025	BE993025	UI-M-B21-
c 869	18	2.5	293	10	BB180870	BB180870	BB180870	926	18	2.5	320	9	AV348729	AV348729	AV348729
870	18	2.5	294	10	BB488570	BB488570	BB488570	927	18	2.5	321	10	BB378811	BB378811	BB378811
871	18	2.5	294	14	CD409035	CD409035	Gm.CK4582	928	18	2.5	321	10	BE368872	BE368872	601221506
c 872	18	2.5	296	10	AW129326	AW129326	w159g07.k	929	18	2.5	322	9	AAU224690	AAU224690	AAU224690
c 873	18	2.5	296	10	AW134864	AW134864	UI-H-B11-	930	18	2.5	323	10	BB390958	BB390958	BB390958
c 874	18	2.5	296	28	AA474209	AA474209	IM0290N01	931	18	2.5	324	9	AT1836044	AT1836044	UI-M-AQ0-
c 875	18	2.5	297	9	AV325944	AV325944	AV325944	932	18	2.5	324	12	B1019153	B1019153	IL3-MN026
c 876	18	2.5	297	10	BB063188	BB063188	BB063188	933	18	2.5	324	13	BY687833	BY687833	BY687833
c 877	18	2.5	298	9	A161832	A161832	w55B805..x	934	18	2.5	324	14	N22723	N22723	y646003.s1
878	18	2.5	298	10	BB023785	BB023785	BB023785	935	18	2.5	325	10	BB453222	BB453222	BB453222
c 879	18	2.5	299	10	BB181842	BB181842	BB181842	936	18	2.5	325	10	BB521151	BB521151	BB521151
880	18	2.5	299	10	BB387397	BB387397	BB387397	937	18	2.5	326	10	BB376333	BB376333	BB376333
881	18	2.5	300	10	BB027769	BB027769	BB027769	938	18	2.5	326	12	BG940166	BG940166	BG940166
882	18	2.5	300	10	BB417605	BB417605	BB417605	939	18	2.5	326	13	CG300918	CG300918	CG300918
883	18	2.5	300	10	BB487228	BB487228	BB487228	940	18	2.5	327	14	CD068932	CD068932	CD068932
c 884	18	2.5	300	28	BH195169	BH195169	TC3-71H3.	941	18	2.5	327	14	BE651751	BE651751	UI-M-AQ0-
c 885	18	2.5	301	9	A1721238	A1721238	as68d11.x	942	18	2.5	328	10	BB141985	BB141985	BB141985
886	18	2.5	301	10	BB393770	BB393770	BB393770	943	18	2.5	329	10	BB724754	BB724754	BB724754
c 887	18	2.5	301	14	CB844144	CB844144	RF02.1371	944	18	2.5	330	10	H65036	H65036	y669e11.s1
888	18	2.5	302	10	BB381699	BB381699	BB381699	945	18	2.5	330	14	AA233850	AA233850	RPCT-23-9
889	18	2.5	302	13	C21343	C21343	HUMGS00366	946	18	2.5	331	10	BF580707	BF580707	7H9f02.x
890	18	2.5	303	9	AV327724	AV327724	AV327724	947	18	2.5	332	9	AA669062	AA669062	ab92f07.s
891	18	2.5	304	9	AV220356	AV220356	AV220356	948	18	2.5	332	9	A1365511	A1365511	qk95g06.x
c 892	18	2.5	304	10	BF755841	BF755841	CM3-C1057	949	18	2.5	332	9	AU000976	AU000976	AU000976
c 893	18	2.5	304	10	AW148360	AW148360	x113e12..x	950	18	2.5	332	9	AV139836	AV139836	AV139836
894	18	2.5	305	9	AV368441	AV368441	AV368441	951	18	2.5	332	10	BB461929	BB461929	BB461929
895	18	2.5	305	12	BG940165	BG940165	AK04a02..f	952	18	2.5	332	10	BE424234	BE424234	WH00077.H
c 896	18	2.5	306	10	BB831839	BB831839	RC4-CR007	953	18	2.5	333	10	BF007460	BF007460	1472185.A
897	18	2.5	306	12	BG219027	BG219027	RS138777	954	18	2.5	333	14	W38972	W38972	zb28d10..r1
c 898	18	2.5	306	12	B1522978	B1522978	603175494	955	18	2.5	335	9	AA723509	AA723509	zg71h09.s
c 899	18	2.5	306	12	B1694034	B1694034	603342220	956	18	2.5	335	9	AA723509	AA723509	zg71h09.s

957	18	2.5	336	9	AI207957	AI207957 ap14h10.x
c 958	18	2.5	336	9	AI974127	AI974127 km49411.x
c 959	18	2.5	336	12	BI594058	BI594058 Ag_L3_096
960	18	2.5	336	12	BM738886	BM738886 K-EST0010
961	18	2.5	336	13	BU343332	BU343332 604170795
962	18	2.5	336	14	CM092647	CM092647 G090P27.3
963	18	2.5	337	14	AV546459	AV546459 AV546459
964	18	2.5	337	14	CF979676	CF979676 rgr7811.Y
965	18	2.5	338	13	BY622753	BY622753 BY622753
966	18	2.5	339	10	BB691174	BB691174 BB691174
967	18	2.5	339	13	BY476722	BY476722 BY476722
c 968	18	2.5	341	9	AM024834	AM024834 m696f02.x
969	18	2.5	342	12	BM739879	BM739879 K-EST0010
970	18	2.5	342	13	BY687268	BY687268 BY687268
971	18	2.5	343	10	BB693929	BB693929 BB693929
972	18	2.5	344	10	AA415583	AA415583 49964 MAR
973	18	2.5	344	10	BF007022	BF007022 1418518 A
974	18	2.5	344	14	H88835	H88835 ym26d10.r1
975	18	2.5	346	12	BM827096	BM827096 K-EST0099
976	18	2.5	348	13	BY608650	BY608650 BY608650
c 977	18	2.5	349	28	A4471781	A4471781 1M0286020
c 978	18	2.5	352	9	AA487820	AA487820 ab12404.r
c 979	18	2.5	352	10	AA972126	AA972126 EST184110
980	18	2.5	352	10	BE117589	BE117589 UI-R-BS1-
c 981	18	2.5	353	10	AW126161	AW126161 N1000066
982	18	2.5	353	14	Z34997	Z34997 ATTS3636 St
c 983	18	2.5	354	12	BM115108	BM115108 L08156033
c 984	18	2.5	354	28	BM739915	BM739915 gf21f04.b
985	18	2.5	354	29	DR33H215	DR33H215 DM10 rer
986	18	2.5	355	9	AI147069	AI147069 ok33b12.s
987	18	2.5	355	9	AI661861	AI661861 m53d404.x
988	18	2.5	355	9	AV683509	AV683509 AV683509
989	18	2.5	355	9	AV694237	AV694237 AV694237
990	18	2.5	355	10	AW870748	AW870748 ra50a10.y
991	18	2.5	355	13	BY478834	BY478834 BY478834
c 992	18	2.5	355	14	CB855797	CB855797 r143f11.y
993	18	2.5	357	13	BY497382	BY497382 BY497382
994	18	2.5	357	13	BY698826	BY698826 BY698826
c 995	18	2.5	358	28	AA003450	AA003450 CIT-HSP-2
996	18	2.5	359	9	AV759380	AV759380 AV759380
c 997	18	2.5	359	28	BH012535	BH012535 TD6AK67TH
998	18	2.5	360	13	BY497159	BY497159 BY497159
c 999	18	2.5	361	10	AW514202	AW514202 h475a07.x
c1000	18	2.5	361	12	BM659604	BM659604 CTM602768

ALIGNMENTS

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RESULT 1
BE115451/c
LOCUS BE115451 407 bp mRNA
DEFINITION UI-R-BS1-aww-a-04-0-UI .a1 UI-R-BS1 Ratius
            UI-R-BS1-aww-a-04-0-UI 3', mRNA sequence.
VERSION BE115451
ACCESSION BE115451
KEYWORDS EST.

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SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	1 (bases 1 to 407)
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road / 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA=Yes.
FEATURES	Location/Qualifiers
source	1..407
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	/db_xref="taxon:10116"
	/clone="UI-R-BS1-aww-a-04-0-UI"
	/dev_stage="embryonic 13 dpc"
	/lab_host="DH10B (Life technologies)"
	/clone_lib="UI-R-BS1"
	/note="Vector: pRT13D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS1 library is derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. TAG_TISSUE=embryo at 13 dpc TAG_LIB=UI-R-BS1 TAG_SEQ=AATCC"
ORIGIN	
Query Match	3.2%; Score 23; DB 10; Length 407;
Best Local Similarity	100.0%; Pred. No. 11;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q7	618 CCAAAATTTAAATCCAGTA 640
DB	201 CCAAAATTTAAATCCAGTA 179

RESULT 2
 A2263506/c 420 bp DNA linear GSS 26-JUL-2000
 LOCUS RPCI-23-115K4.TV RPCI-23 Mus musculus genomic clone RPCI-23-115K4,
 DEFINITION genomic survey sequence.
 ACCESSION A2263506
 VERSION A2263506.1 GI:9473833
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatman,S.,
 Akincic,B., Levine,M., McGinn,S., Tsagaye,G., Geer,K., Krol,M., de
 Jong,P. and Fraser,C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSs: RPCI-23-115K4.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: zshao@tifgr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jeong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
 or from Ressea ch Genetics (info@resgen.com). BAC end page:
 http://www.tifgr.org/tbdb/bac_ends/mouse/bac_end_intro.html
 Plate: 115 row: K column: 4
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-115K4"
 /sex="Female"
 /lab_host="DH10B"
 /clone_id="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACs3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Site
 selected DNA was cloned into the pBACs3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 ORIGIN
 Query Match 3.2%; Score 23; DB 26; Length 420;

Best Local Similarity 100.0%; Pred. No. 11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 532 AAGGTAAAAAATTTAAAGTAA 554
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 DB 410 AAGGTAAAAAATTTAAAGTAA 388
 RESULT 3
 B2728592 687 bp DNA linear GSS 03-MAR-2003
 LOCUS OGFBS50TM_ZM_0.7_1.5_KB zea mays genomic clone ZMBSH245103,
 DEFINITION genomic survey sequence.
 ACCESSION B2728592
 VERSION B2728592.1 GI:28701840
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 687)
 REFERENCE Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Buddman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 COMMENT Other_GSSs: OGFBS50TC
 Contact: Cathy Whiteley
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteley@tifgr.org
 Seq primer: TR
 Class: sheared ends.
 FEATURES
 source Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBSH245103"
 /clone_id="ZM_0.7_1.5_KB"
 /note="Vector: pBSK-; Site_1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 ORIGIN
 Query Match 3.2%; Score 23; DB 26; Length 687;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 325 TATTATTAGATTGTTTAA 347
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 DB 646 TATTATTAGATTGTTTAA 668

RESULT 4
CG094526/c 805 bp DNA linear GSS 20-AUG-2003

LOCUS
DEFINITION PUF7B71TB ZM_0.6.1.0_KB Zea mays genomic clone ZMWBta0726L22,
genomic survey sequence.

ACCESSION
CG094526

VERSION
CG094526.1 GI:33976820

KEYWORDS
GSS.

SOURCE
Zea mays

ORGANISM
Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bernetzen,J.

TITLE
Maize Genomics Consortium

JOURNAL
Unpublished (2003)

COMMENT
Other GSSs: PUF7B71TB
Contact: Cathy Whitelaw

FEATURES
source
Location/Qualifiers
1..805
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBta0726L22"
/clone_lib="ZM_0.6.1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 3.2%; Score 23; DB 29; Length 805;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 AAATTGAAAATAATTAATAA 492
|||||

DB 315 AAATTGAAAATAATTAATAA 293

RESULT 5
CG060667/c 821 bp DNA linear GSS 19-AUG-2003

LOCUS
DEFINITION PUCW74TD ZM_0.6.1.0_KB Zea mays genomic clone ZMWBta0639N03,
genomic survey sequence.

ACCESSION
CG060667

VERSION
CG060667.1 GI:33932847

KEYWORDS
GSS.

SOURCE
Zea mays

ORGANISM
Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bernetzen,J.

TITLE
Maize Genomics Consortium

JOURNAL
Unpublished (2003)

COMMENT
Other GSSs: PUCW74TB
Contact: Cathy Whitelaw

FEATURES
source
Location/Qualifiers
1..821
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBta0639N03"
/clone_lib="ZM_0.6.1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 3.2%; Score 23; DB 29; Length 821;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 AAATTGAAAATAATTAATAA 492
|||||

DB 269 AAATTGAAAATAATTAATAA 247

RESULT 6
CG094522 869 bp DNA linear GSS 20-AUG-2003

LOCUS
DEFINITION PUF7B71TB ZM_0.6.1.0_KB Zea mays genomic clone ZMWBta0726L22,
genomic survey sequence.

ACCESSION
CG094522

VERSION
CG094522.1 GI:33976816

KEYWORDS
GSS.

SOURCE
Zea mays

ORGANISM
Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bernetzen,J.

TITLE Bennetzen, J.
JOURNAL Maize Genomics Consortium
COMMENT Unpublished (2003)
Other_GSSs: PUF7B71TD
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 7F
Class: sheared ends.

FEATURES
source location/Qualifiers
1..869
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBTA0726L22"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 3.2%; Score 23; DB 29; Length 869;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 AAATGAAATTAATTAATAA 492
|||||
Db 787 AAATGAAATTAATTAATAA 809

RESULT 7
CG083261 913 bp DNA linear GSS 20-AUG-2003
LOCUS PUFQD39TB ZM_0.6_1.0_KB Zea mays genomic clone ZMWBTA0707H06,
DEFINITION genomic survey sequence.
ACCESSION CG083261 GI:33965555
VERSION CG083261.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 913)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Reenick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUFQD39TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843

FEATURES
source location/Qualifiers
1..913
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBTA0707H06"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 3.2%; Score 23; DB 29; Length 913;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 AAATGAAATTAATTAATAA 492
|||||
Db 689 AAATGAAATTAATTAATAA 711

RESULT 8
CG204442/c 913 bp DNA linear GSS 21-AUG-2003
LOCUS PUCJ85TD ZM_0.6_1.0_KB Zea mays genomic clone ZMWBTA0639001,
DEFINITION genomic survey sequence.
ACCESSION CG204442
VERSION CG204442.1 GI:34095503
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 913)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Reenick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUCJ85TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 7F
Class: sheared ends.

FEATURES
source location/Qualifiers
1..913
/organism="Zea mays"
/mol_type="genomic DNA"

/strain="973"
/db_xref="taxon:4577"
/clone="ZM67a063901"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 3.2%; Score 23; DB 29; Length 913;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 AAATGAAATTAATTAATTA 492
DB 269 AAATGAAATTAATTAATTA 247

RESULT 9

CG083259/c 940 bp DNA linear GSS 20-AUG-2003
LOCUS PUFQD39TB ZM.0.6.1.0.KB Zee mays genomic clone ZM67a0707H06,
DEFINITION genomic survey sequence.
ACCESSION CG083259
VERSION CG083259.1 GI:33965593
KEYWORDS GSS.
SOURCE Zee mays
ORGANISM Zee mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Penicillidae; Andropogoneae; Zee.
1 (bases 1 to 940)
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benneken,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQD39TD
Contact: Cathy Whitelaw

REFERENCE

TITLE
JOURNAL
COMMENT

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 7R
Class: sheared ends.

FEATURES

source
1..940
Location/Qualifiers
/organism="Zee mays"
/mol_type="genomic DNA"
/strain="973"
/db_xref="taxon:4577"
/clone="ZM67a0707H06"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 3.2%; Score 23; DB 29; Length 940;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 470 AAATGAAATTAATTAATTA 492
DB 565 AAATGAAATTAATTAATTA 543

RESULT 10

BE184302/c 141 bp mRNA linear EST 22-JUN-2000
LOCUS CM0-HT0674-080500-360-e04 HT0674 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE184302
ACCESSION BE184302
VERSION BE184302.1 GI:8663486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 141)
Dias Neto,E., Garcia Correa,R., Verjovskij-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=4t2=CM0-HT0674-080
500-360-e04t3=2000-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 43
High quality sequence stop: 139.

FEATURES

source
1..141
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="Adulc"
/clone_lib="HT0674"
/note="Organ: head_neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORFESTS PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 3.1%; Score 22; DB 10; Length 141;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 CAAATGATGATGAATAAATGA 233
|||||
56 CAAATGATGATGAATAAATGA 35

RESULT 11

BH040485

LOCUS

DEFINITION

461 bp DNA linear GSS 17-JUL-2001
RPCI-24-300023.TV RPCI-24 Mus musculus genomic clone
RPCI-24-300023, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 461)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akincet, B., Lavins, M.,
Teagay, G., Geor, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-300023.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: zshao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdjong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
Page: http://www.tigr.org/tcd/bac_ends/mouse/bac_end_intro.html
Plate: 300 row: 0 column: 23
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..461
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-300023"
/sex="Male"

/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBA1 cloning vector at the
BamHI sites using MspI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 3.1%; Score 22; DB 28; Length 461;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 ATAAATAGATTAATAATAATA 688
|||||
273 ATAAATAGATTAATAATAATA 294

RESULT 12

AM828209

LOCUS

DEFINITION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

529 bp mRNA linear EST 10-MAY-2001
ra67n08.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
cDNA 5' similar to SW:U14_HUMAN P49917 DNA LIGASE IV; mRNA
sequence.
AM828209
AM828209.1 GI:7921996
EST.
Meloidogyne incognita (southern root-knot nematode)
Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchidae; Heteroderidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 529)
McCarter, J., Clifton, S., Chipell, B., Pope, D., Martin, J.,
Wyllie, T., Dant, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Rutter, E., Bennett, J., Franklin, C.,
Tsagaris, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Pearson, B., Skeller, T.,
Harvey, N., Schurk, R., Kohn, S., Shu, F., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R., and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Uma Rao and David Bird
(david_bird@cau.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center St.
Louis.

Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1..529

FEATURES

source

/organism="Meloidogyne incognita"
/mol_type="mRNA"
/db_xref="taxon:6306"
/dev_stage="enriched for 2nd stage juveniles"
/lab_host="XLRJ"
/clone_lib="Bird-Rao Meloidogyne incognita J2"
/note="Vector: ZAP express - pBKCMV (Stratagene), Site_1:
EcoRI; Site_2: XhoI; Oligo (dT) primed library. cDNA was
constructed and cloned unidirectionally into the vector
within the 5' EcoRI and 3' XhoI sites. This library was
constructed by Dr. Uma Rao and Dr. David Bird at North
Carolina State University."

Query Match 3.1%; Score 22; DB 10; Length 529;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 468 AGAATTGAAATTAATTAAT 489
DB 80 AGAATTGAAATTAATTAAT 101

RESULT 13
B1501692/c 552 bp mRNA linear EST 29-AUG-2001
LOCUS B1501692
DEFINITION rmo3H02.Y1 Meloidogyne arenaria egg PAMPI v1 Chiapelli McCarter
B1501692
VERSION B1501692.1 GI:15352081
KEYWORDS EST.
SOURCE Meloidogyne arenaria
ORGANISM Meloidogyne arenaria
Eukaryote; Metazoa; Nematode; Chromadorea; Tylenchida; Tylenchines;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

REFERENCE
AUTHORS
1 (bases 1 to 552)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaaba, T., Theisling, B.,
Bowers, Y., Gibbons, M., Rlter, E., Bennett, J., Franklin, C.,
Tsagarolashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Smaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCamy, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter, J.P.
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
(bchiapelli@wustl.edu & jmcarter@wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center, St. Louis. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North Carolina

State University.
High quality sequence stop: 427.
FEATURES
source
1..552
Location/Qualifiers
/organism="Meloidogyne arenaria"
/mol_type="mRNA"
/db_xref="taxon:6304"
/dev_stage="egg"
/lab_host="DH10B"
/clone_lib="Meloidogyne arenaria egg PAMPI v1 Chiapelli
McCarter"

/note="Vector: PAMPI (Gibco); Site_1: NotI; Site_2: SalI;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
cDNA was made by using Dynabead oligo-dT priming (Dyna1).
PCR based library using a modified protocol from the
SMART PCR cDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of PAMPI. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North
Carolina State University."

Query Match 3.1%; Score 22; DB 12; Length 552;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 468 AGAATTGAAATTAATTAAT 489
DB 224 AGAATTGAAATTAATTAAT 203

RESULT 14
BH307917 582 bp DNA linear GSS 30-NOV-2001
LOCUS BH307917
DEFINITION CH230-4J17.TV CHORI-230 segment 1 Rattus norvegicus genomic clone
BH307917, genomic survey sequence.
CH230-4J17, genomic survey sequence.
ACCESSION BH307917.1 GI:17220325
VERSION BH307917.1
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 582)
Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,
Shvartsbeyn, A., Gbregedreg, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-4J17.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pjejong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering-information.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat_bac_end_intro.html
Plate: 4 row: J column: 17
Seq primer: 17

FEATURES

Location/Qualifiers
1..582
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-4J17"
/sex="Female"
/cell_type="Brain"
/clone_id="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCM) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 3.1%; Score 22; DB 28; Length 582;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 476 AAAAAATTAAATTAATTGA 497
|||||
DB 403 AAAAAATTAAATTAATTGA 424

RESULT 15

LOCUS B084733 197 bp mRNA linear EST 29-SEP-2003
DEFINITION B084733 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL100e14 3', mRNA sequence.
ACCESSION B084733
VERSION B084733.1 GI:17580404
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM

REFERENCE

1 (bases 1 to 197)
Kikayama, A., Terashima, C., Mochii, M., Ueno, N., Shin-I, T. and
Kohata, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadao Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-539-81-6856

JOURNAL

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadao Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-539-81-6856

Fax: 81-539-81-6855
Email: tsbni@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.

FEATURES

Location/Qualifiers
1..197
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL100e14"
/class_type="whole embryo"
/dev_stage="stage 25"
/clone_id="NIBB Mochii normalized Xenopus tailbud
library"

ORIGIN

Query Match 2.9%; Score 21; DB 12; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 407 AAAAAACACACGAATTCA 427
|||||
DB 103 AAAAAACACACGAATTCA 123

Search completed: October 15, 2004 06:23:57
Job time: 3410.09 secs